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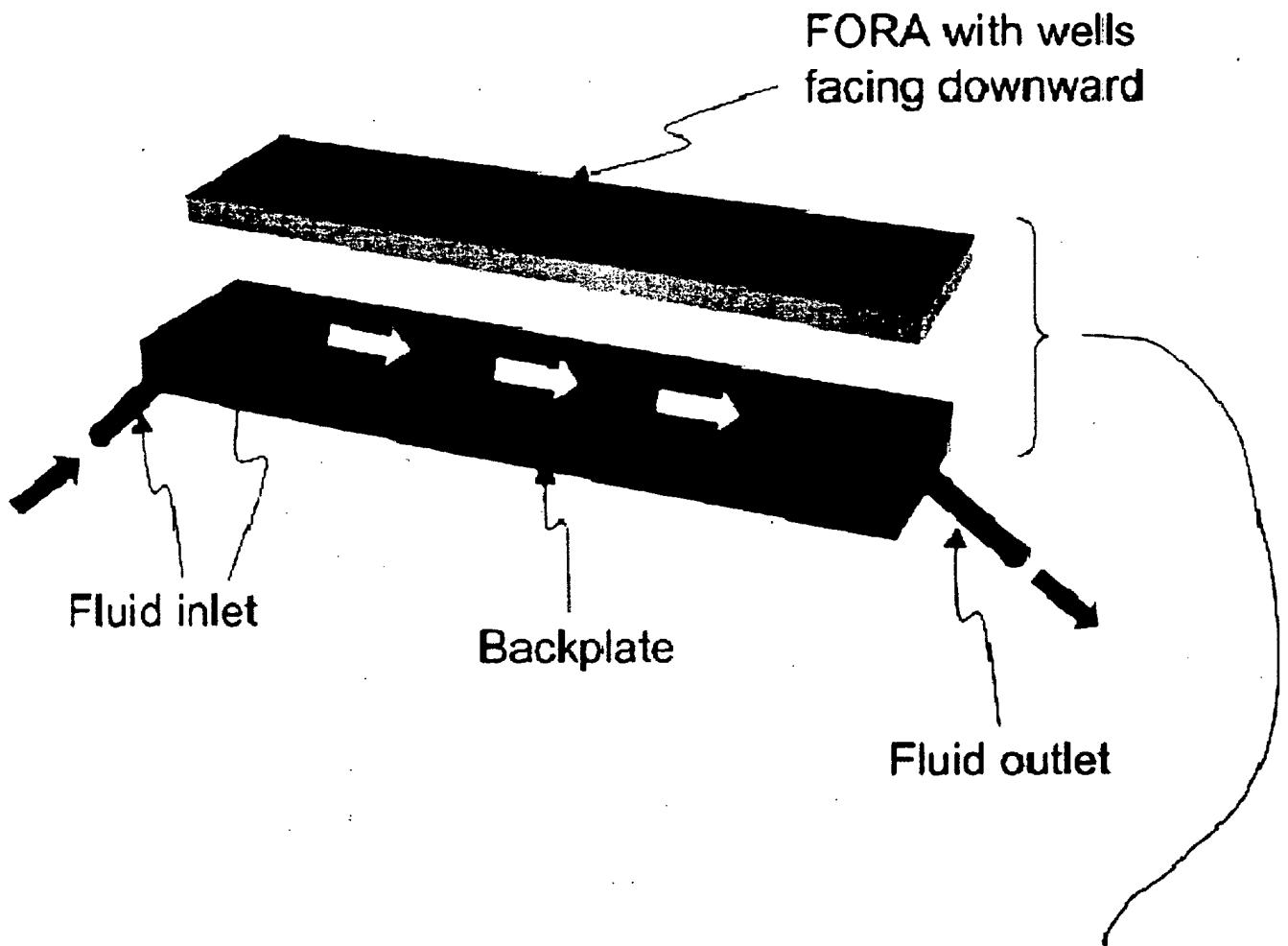
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FORA and back-plate are pressed together with a seal to create a closed flow chamber.

Figure 16

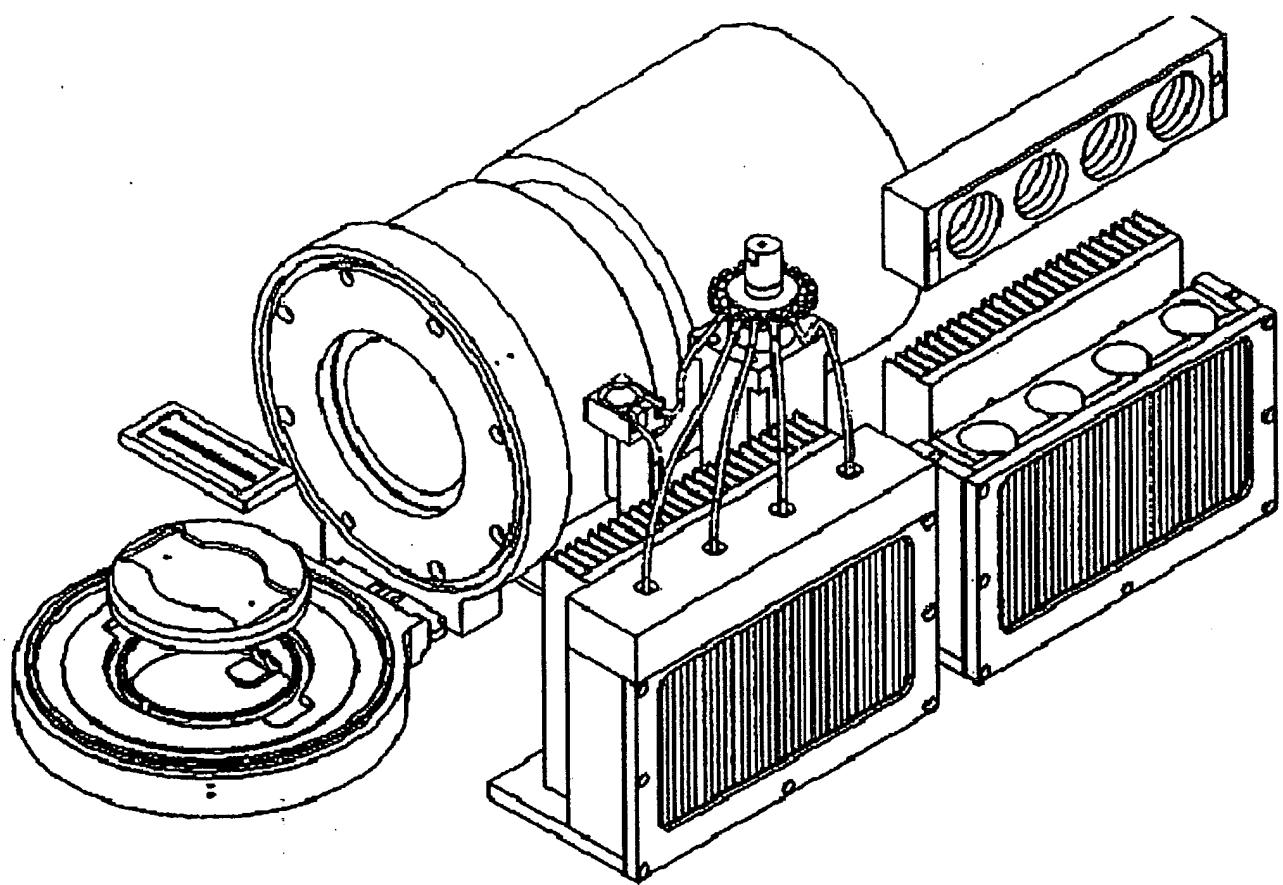


Figure 17

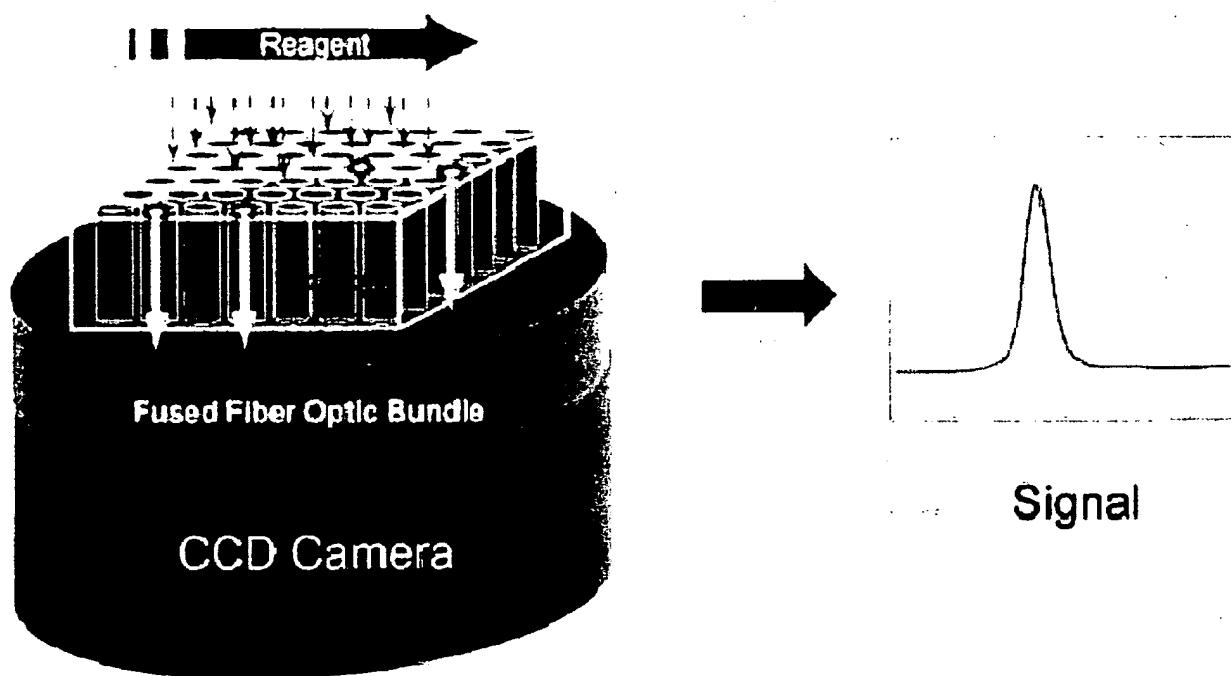
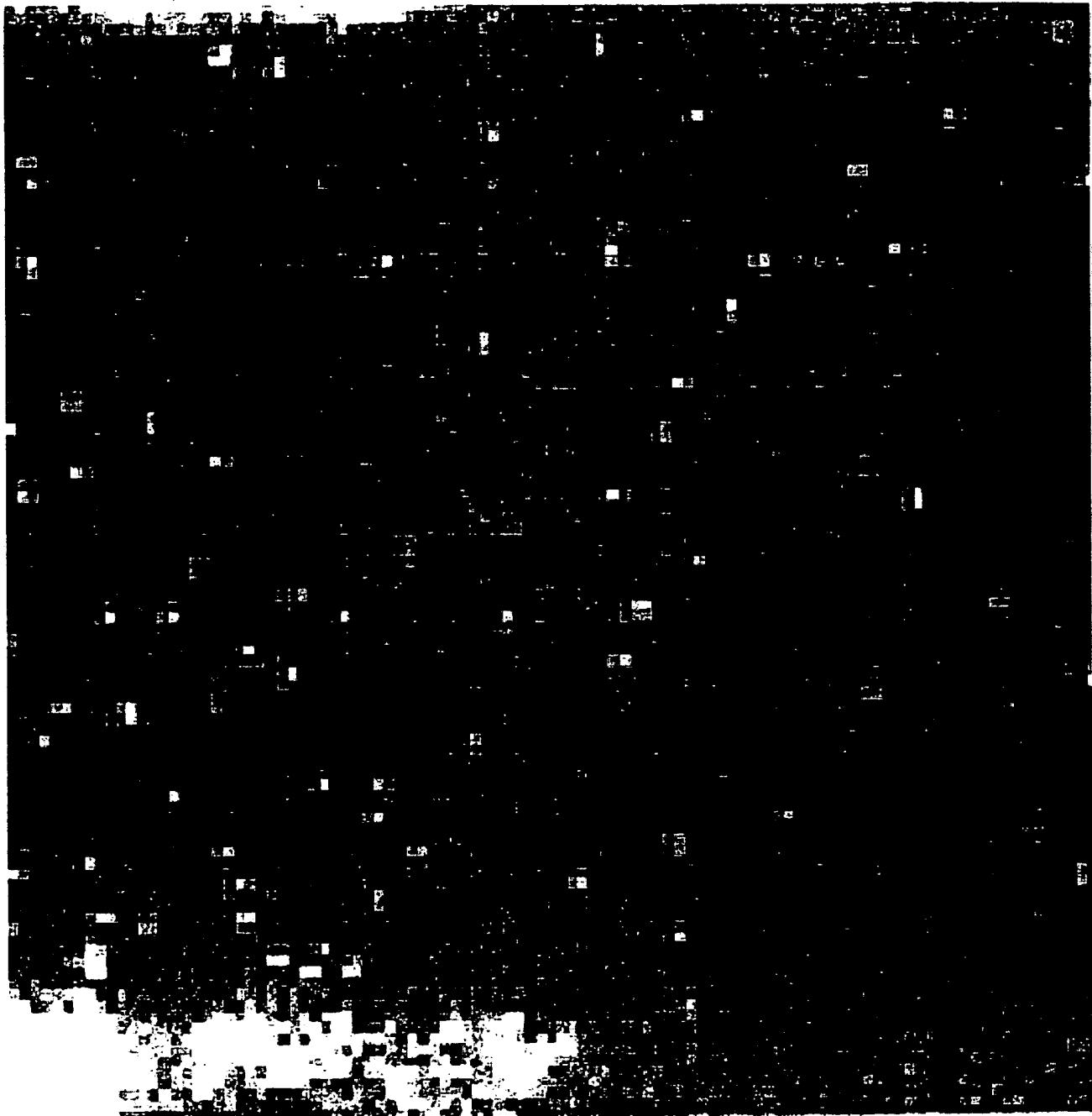


Figure 18



Sulfurylase on mobile support/Luciferase on surface, PPi flows across FORA surface. 1 mobile-support per pixel on camera; 50 $\mu$ m FORA well spanning 4 15 $\mu$ m pixels. Shown is 100 x 100 Pixels (10K pixels), 1.5 mm<sup>2</sup>.

Figure 19

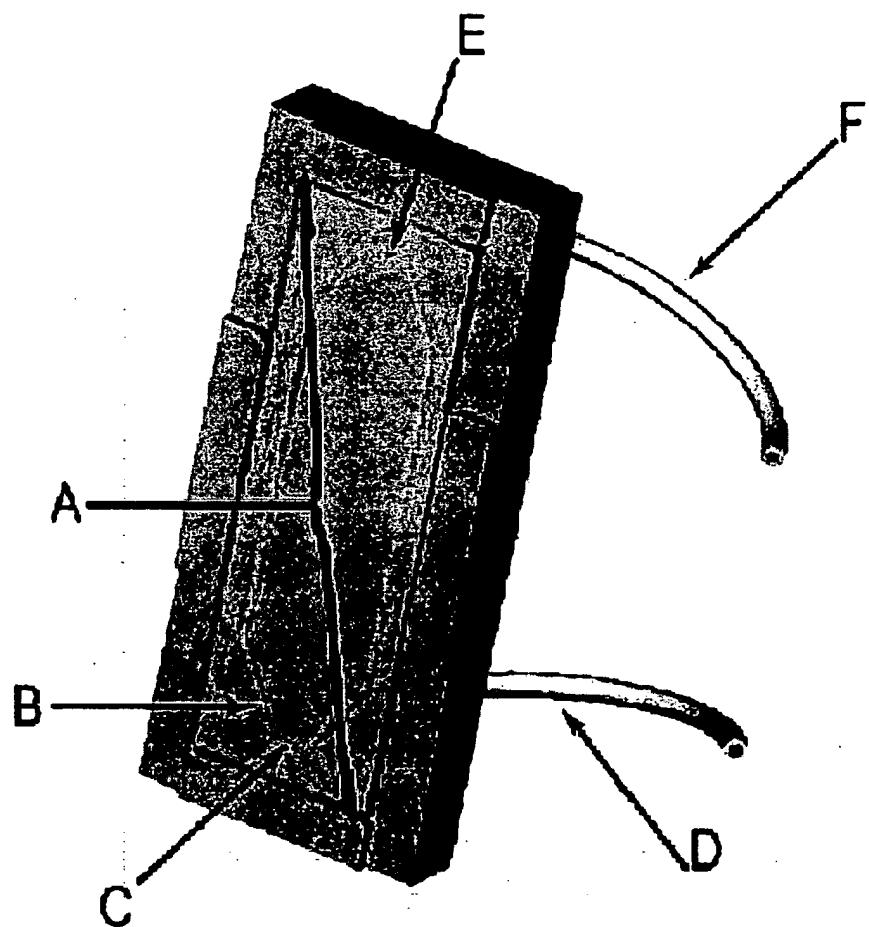


Figure 20

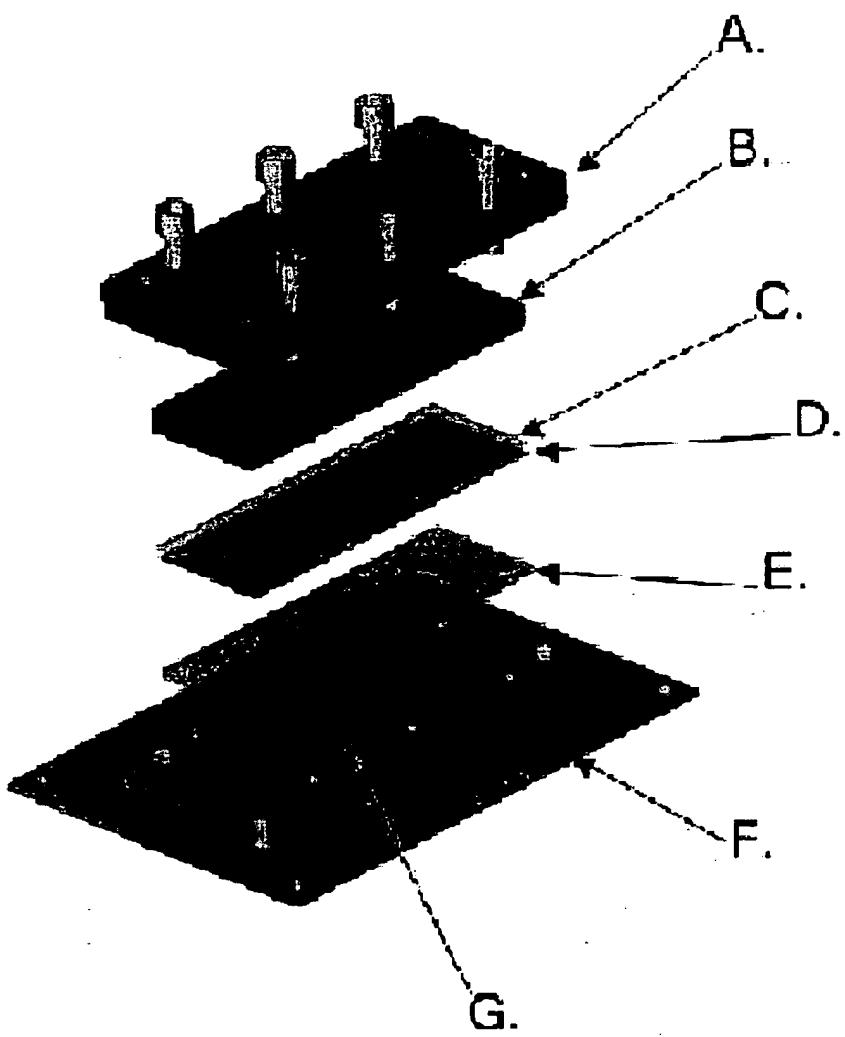


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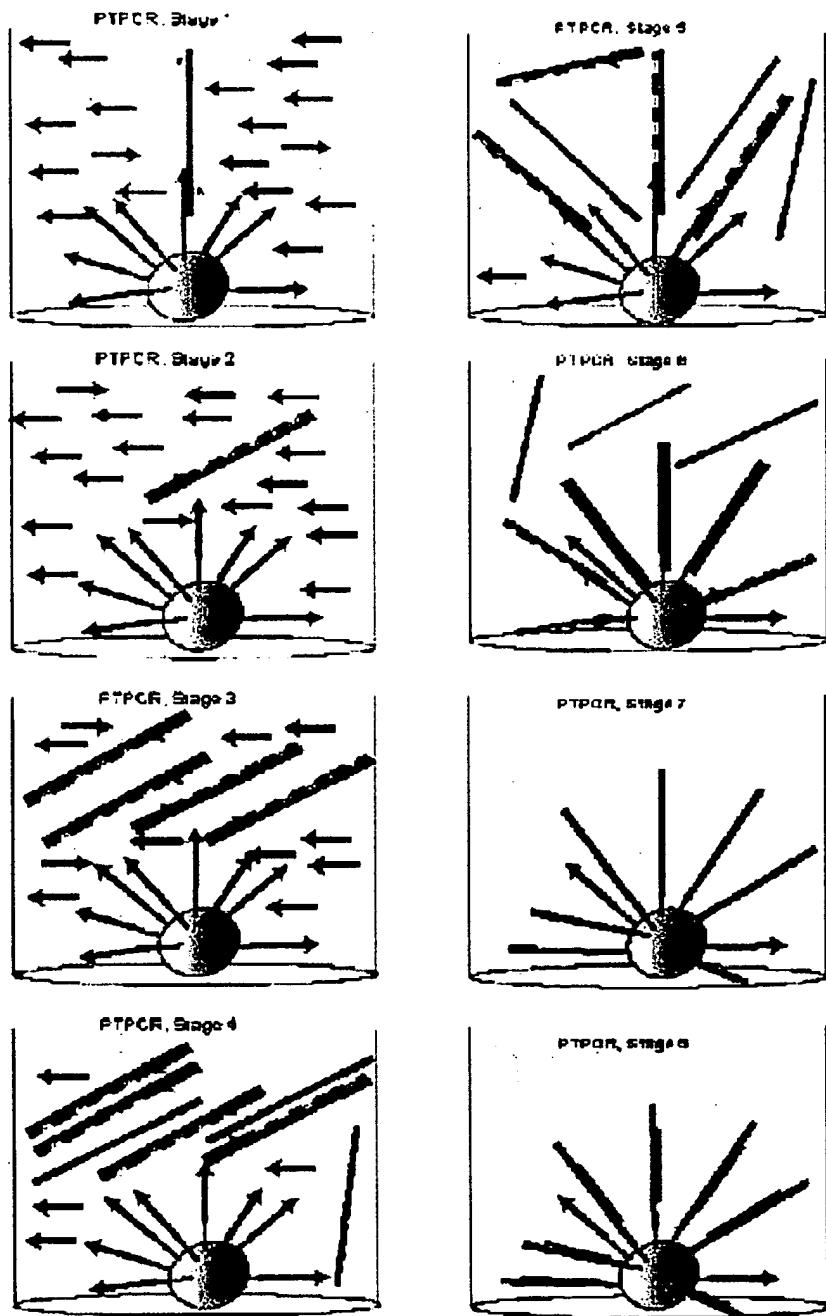
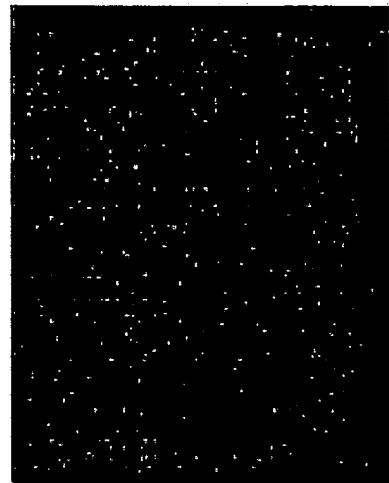
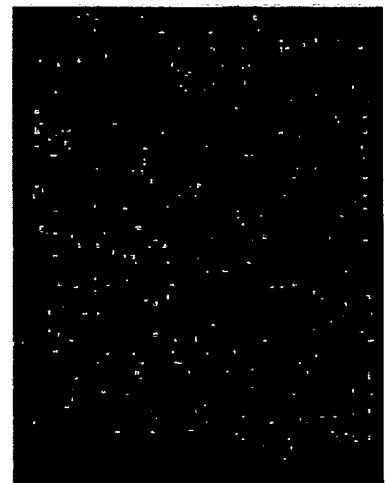


Figure 22

**A**



**B**



**C**



**Figure 23**

Figure 24

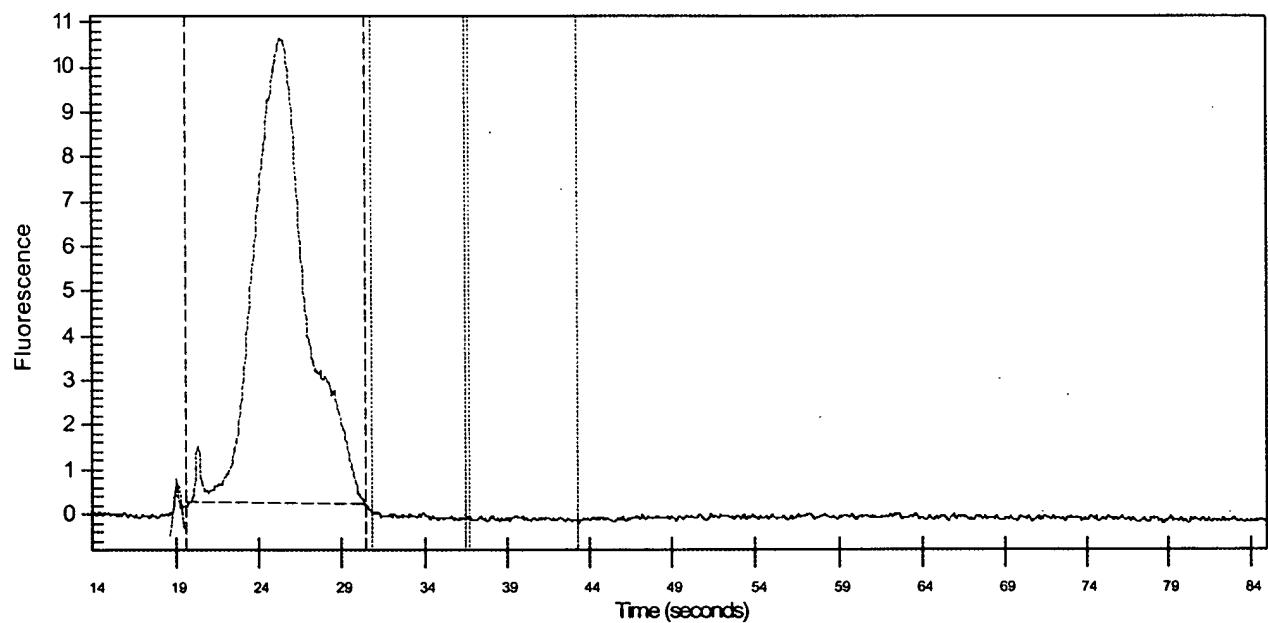
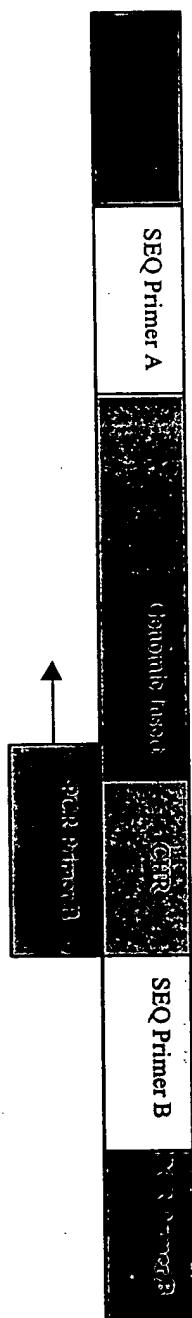


Figure 25

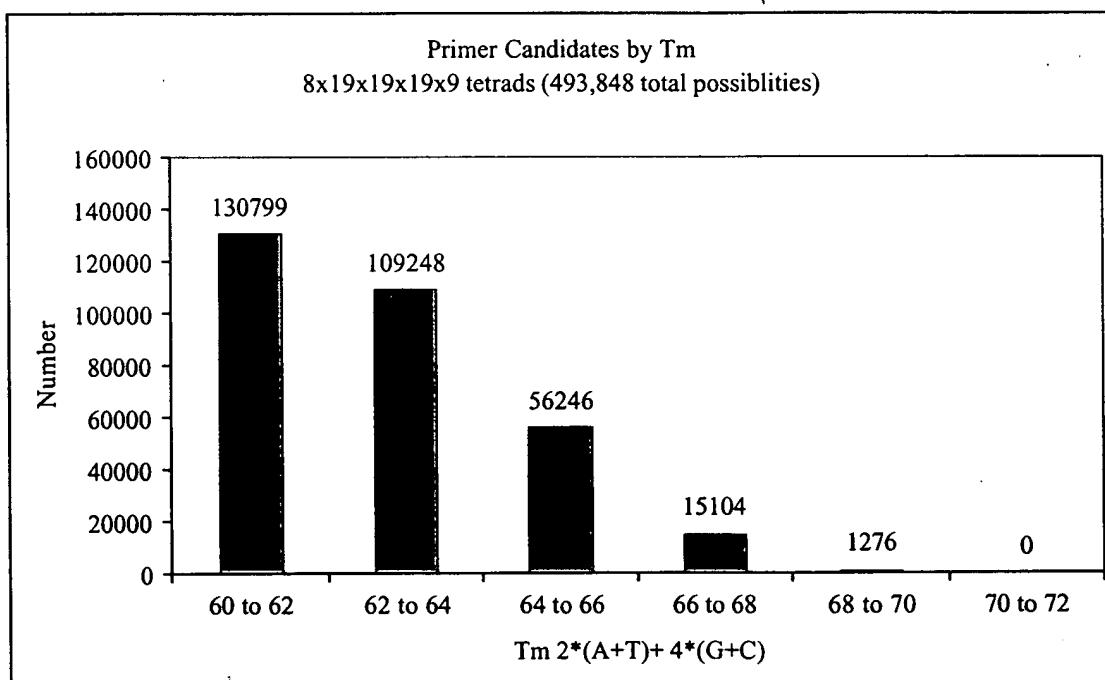
SEQ Primer A	Gemonic losen	SEQ Primer B	SEQ Primer C
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Figure 26



NYC 279372v1

Figure 27



**Figure 28**

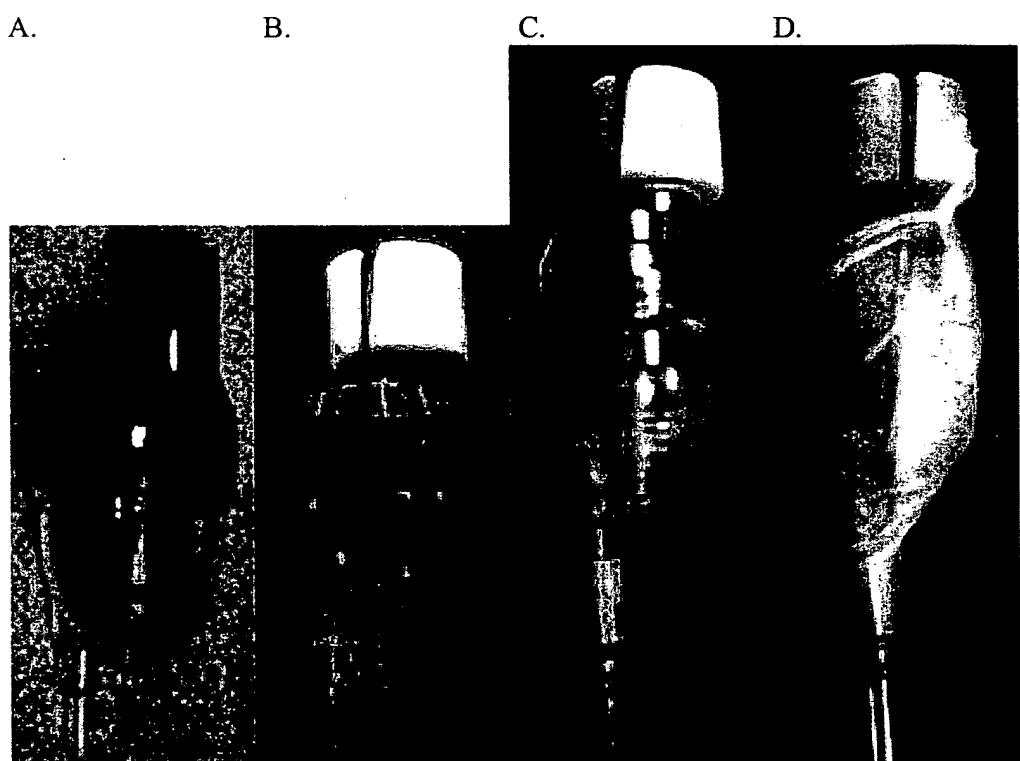


Figure 29A

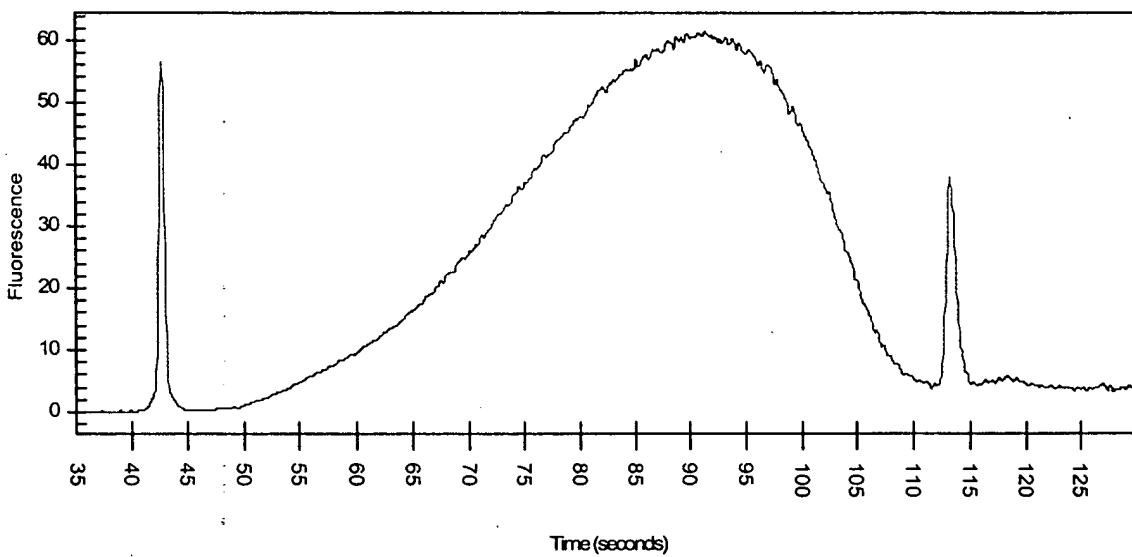
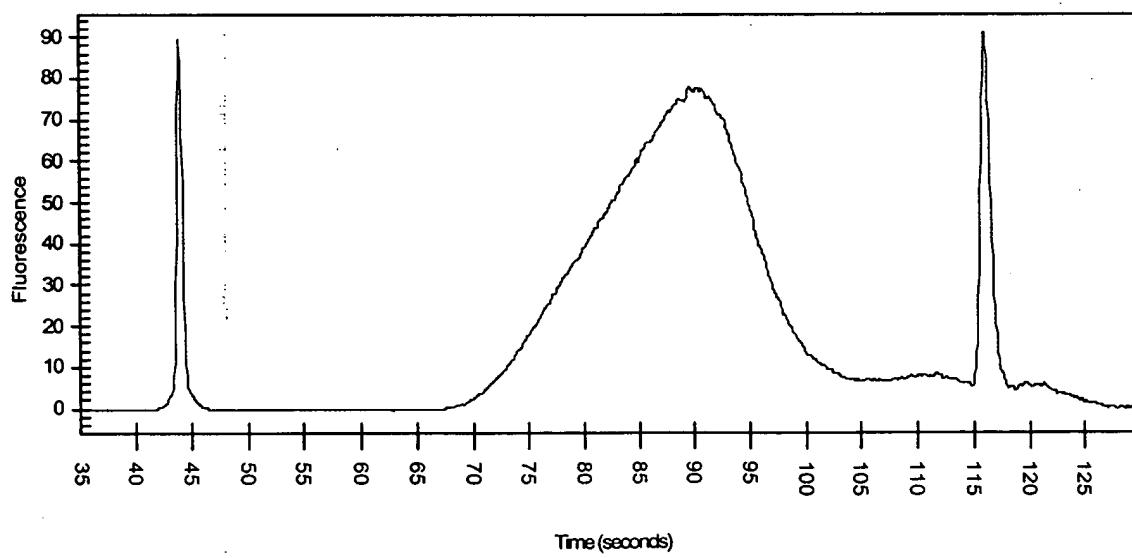


Figure 29B



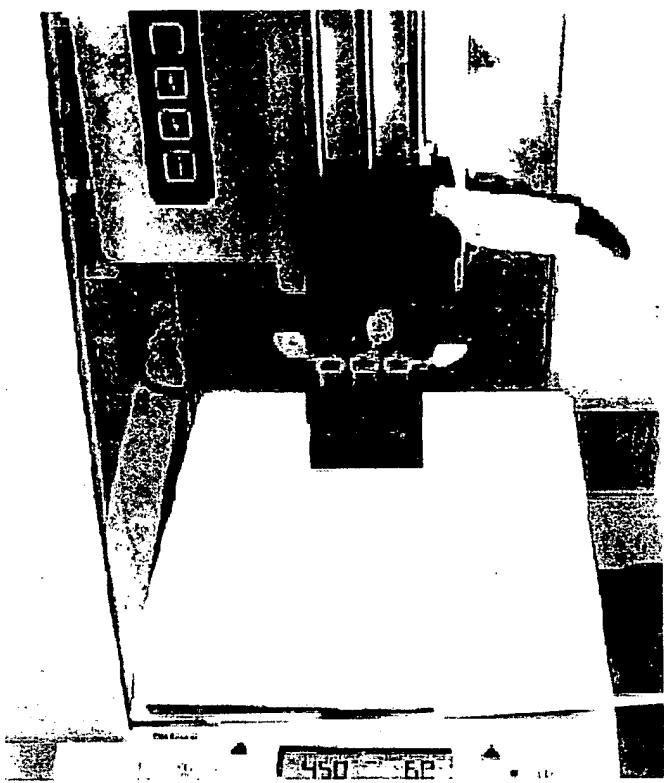


Figure 30

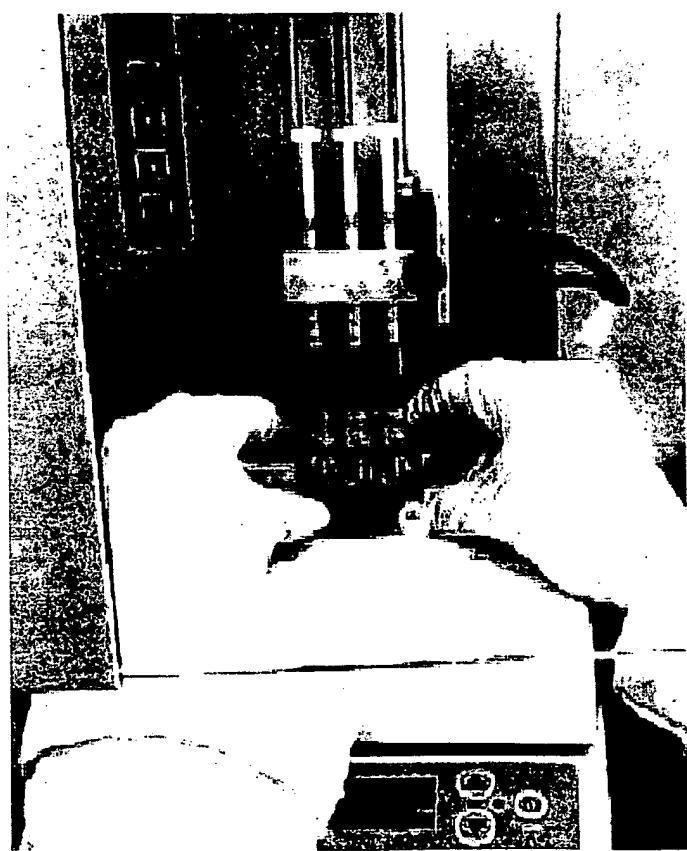


Figure 31

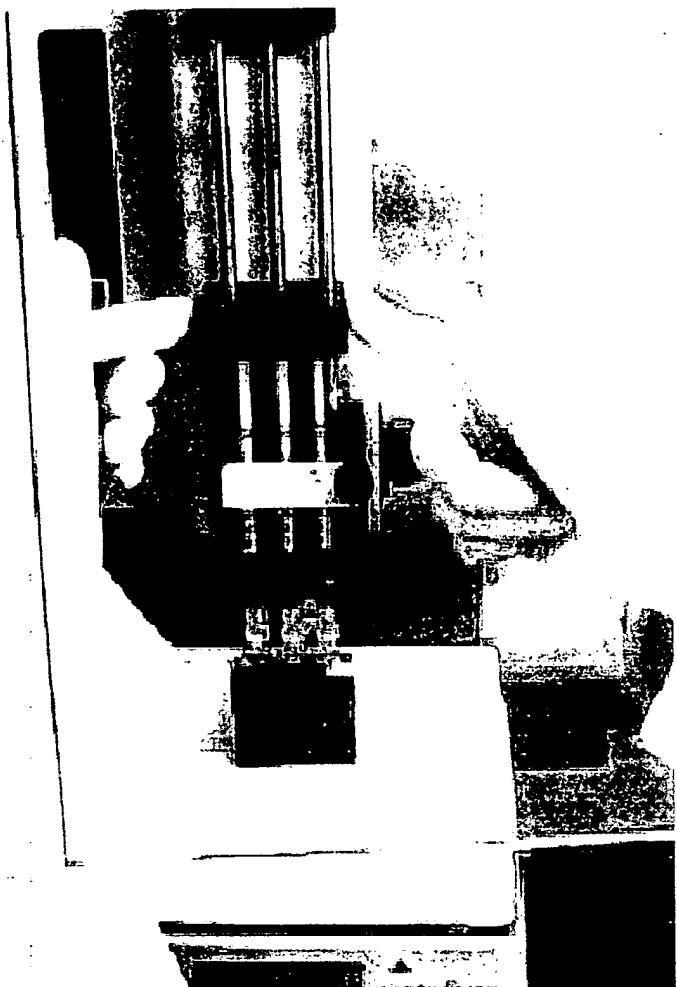


Figure 32

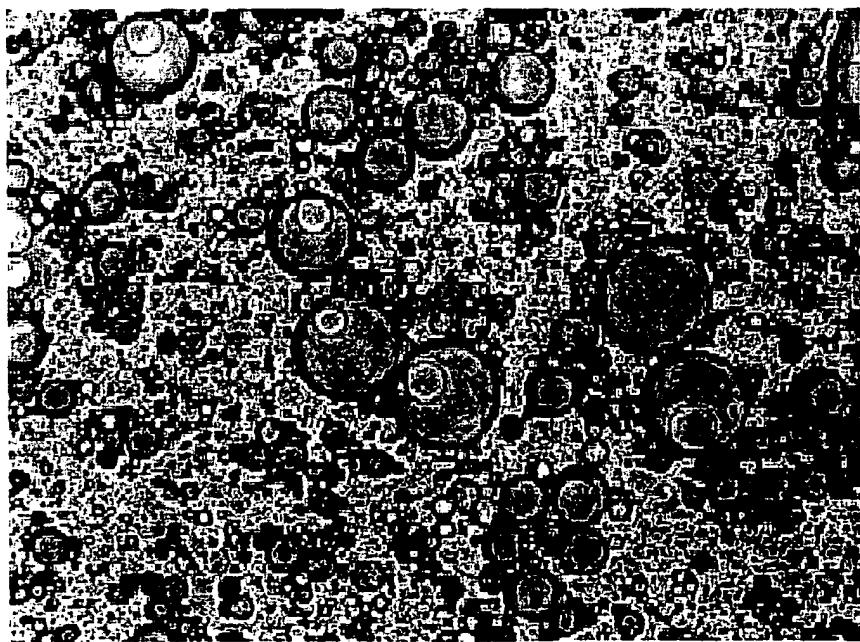


Figure 33

**FIGURE 34**

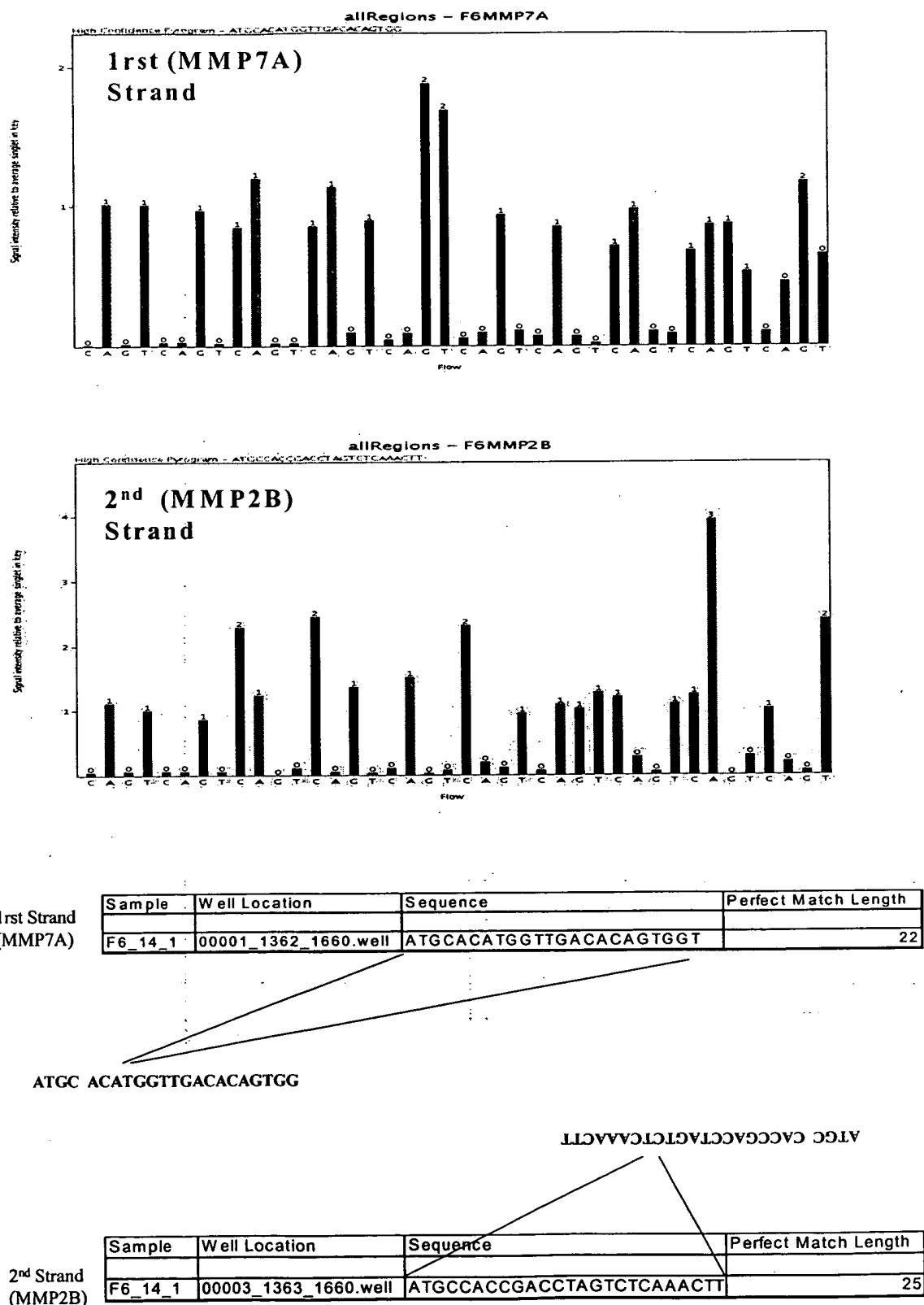


Fig. 35

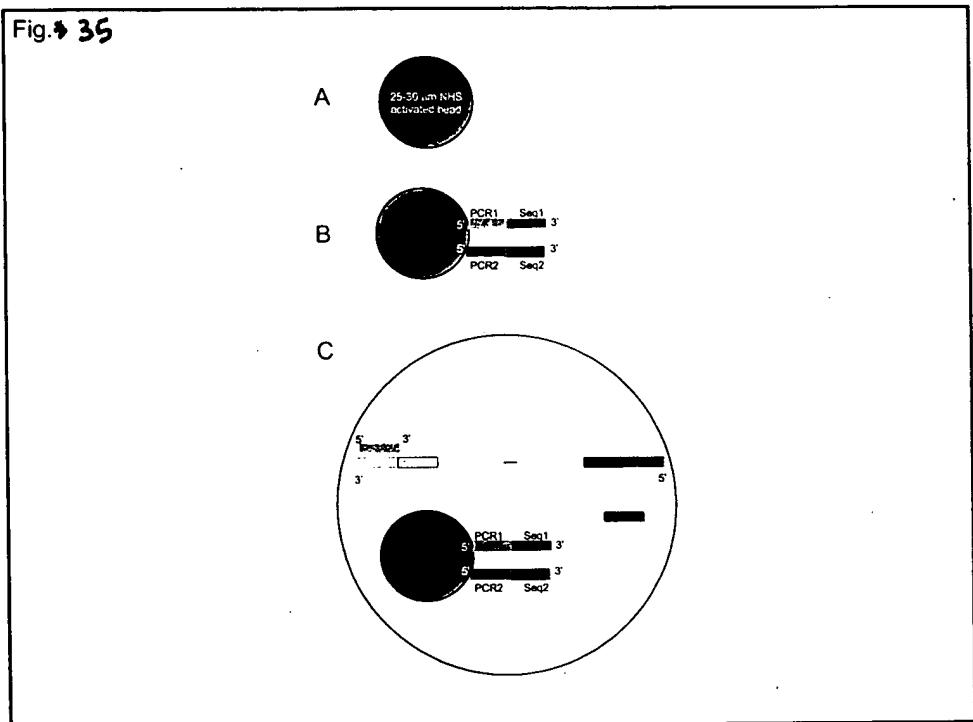


Fig. 36

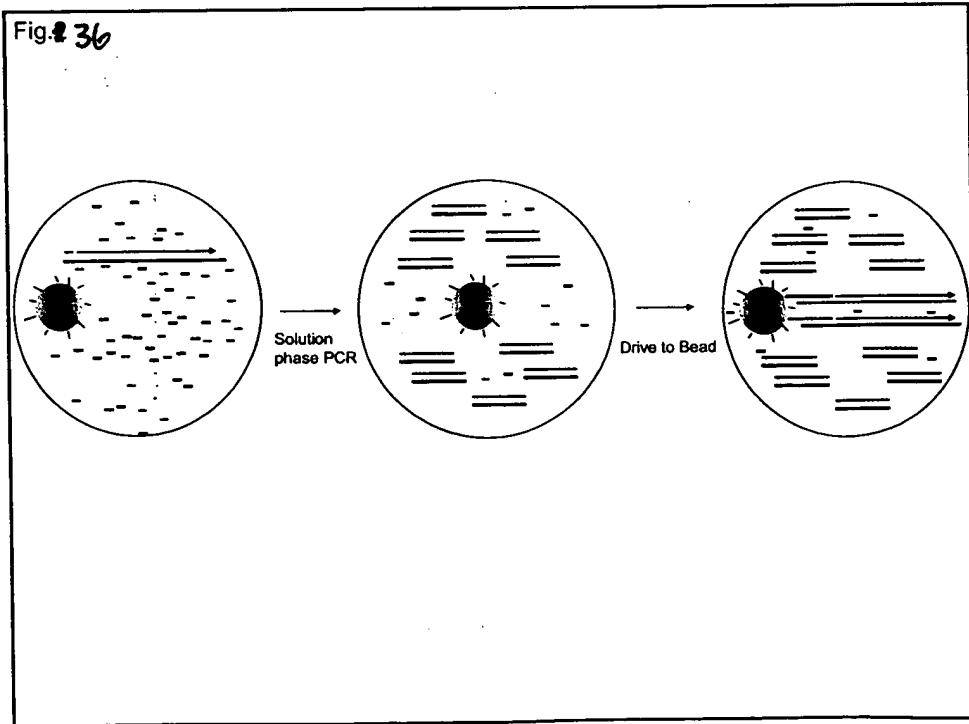


Fig. 37

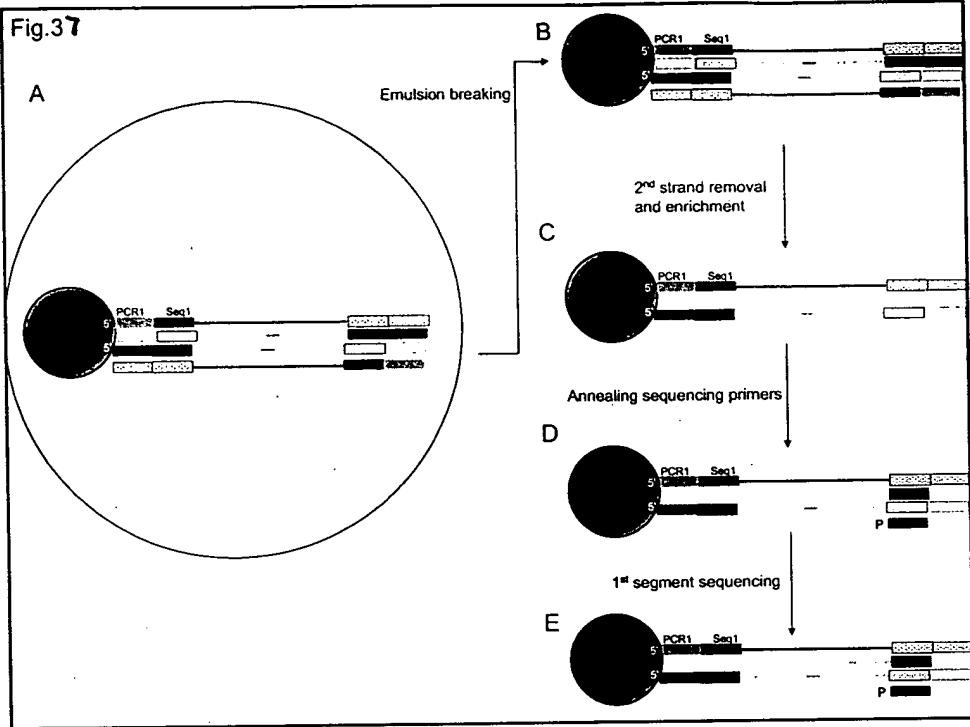


Fig. 38

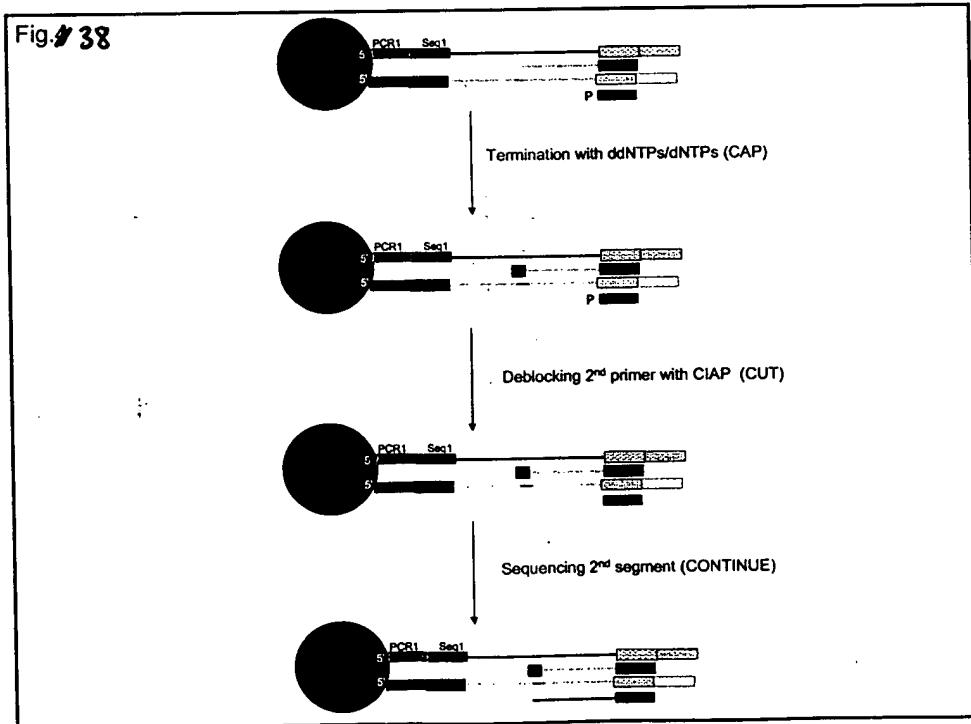


Fig. 39

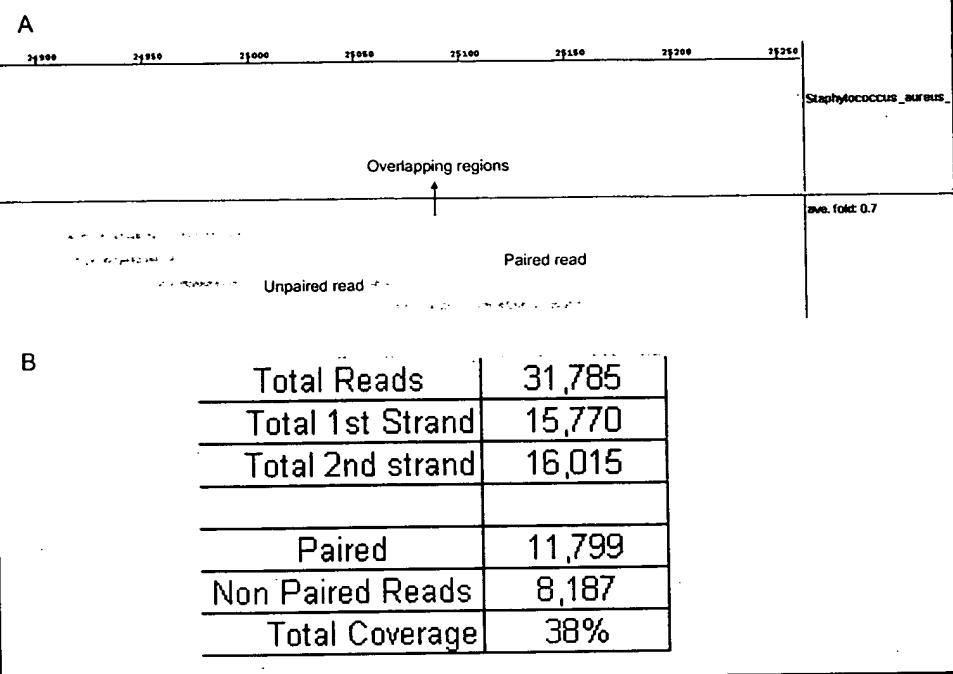


Fig. 40

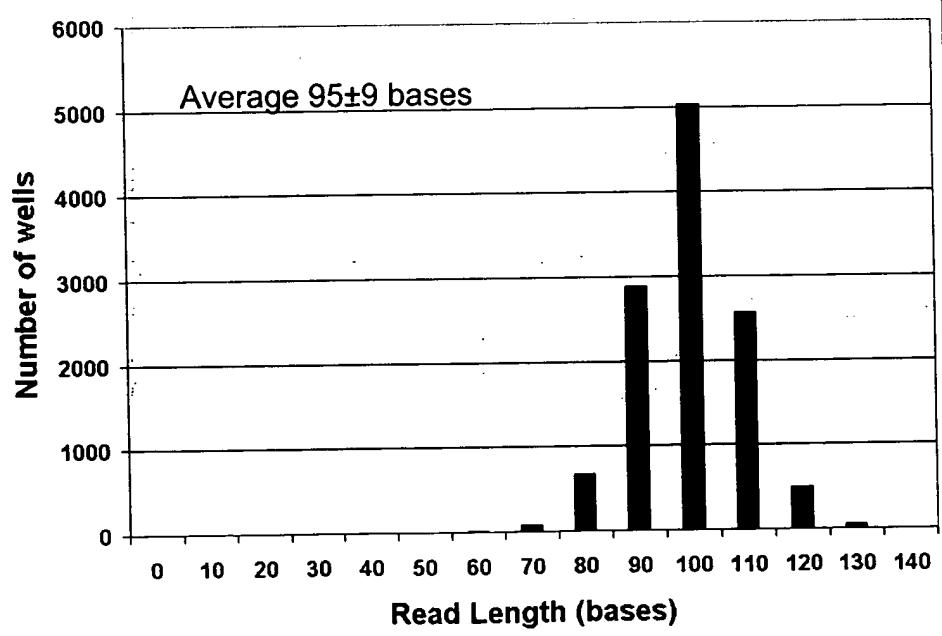


Fig. 41

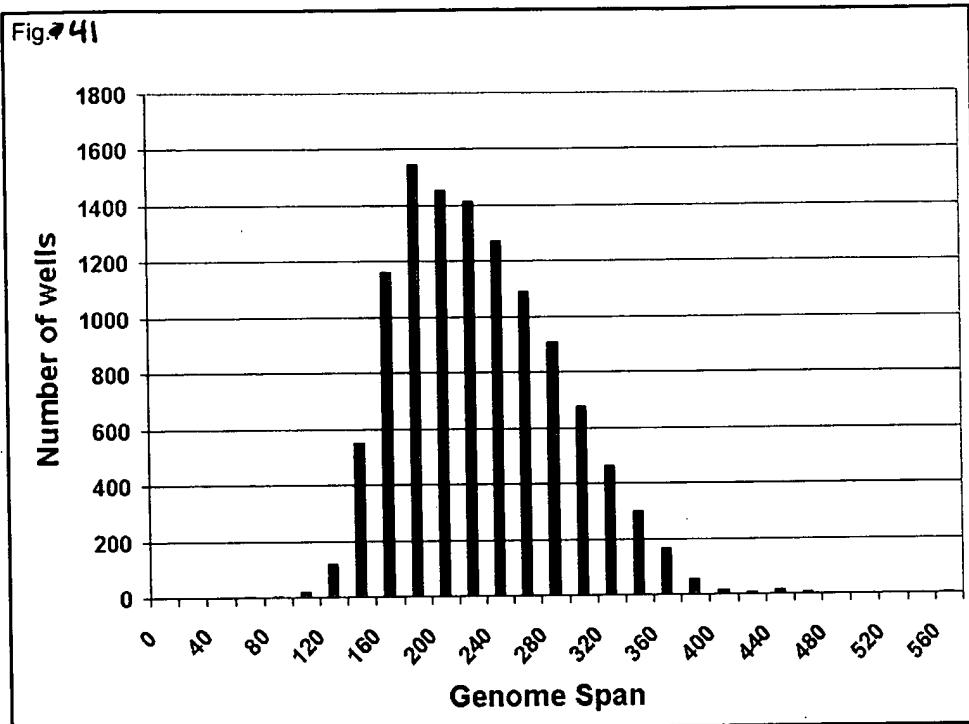


Fig. 42

Well	Genome Position	Orientation	Alignment String
00364_0548_2509	571366	F	TATTGTTGATGCTGTAAGAAAGCTACTGGTGTAGAATTTTATGAAGTT
00364_0548_2509_D2	571512	R	TGCTCAAGAAGATTCAATTAAAATATGACCATATTCTATGTATCTT
00363_0985_2232	1487890	R	AAGCGAACAGTCAGTACCCACAGTCAGTTGACITTAACAAAGCGGAT
00363_0985_2232_D2	1487769	F	TACAGGTGTGGTATGCCATTGCGATTITGCGCTTGGGTTAGCCG
00397_0940_2923	2611033	F	AAACATAAACATCCCCTATCTCAATTCCGCTTCCATGTAAACAAAAAGC
00397_0940_2923_D2	2611164	R	TAGATATCACTTGGTGTACTGGTAATGCAGGCATGAG
00417_0611_1933	122001	R	ATTCAACTCTGGAAATGCCTTCTGATACGCCCTCGATGATG
00417_0611_1933_D2	121930	F	GATGAGGGAGCTGCAATGGCAATGGGTTAAAGGGCATCATCG
00434_0595_0993	2022591	R	TGTATCTGATTGGATTAGTTGCTTTCATCTTATTAGACC
00434_0595_0993_D2	2022473	F	CATTAACATCTGCACCAAGAAATAGCTCTAATACGATTG
00443_1003_0754	107373	F	GCGACGACGTCCACGTAATAACGGCTGCACCTAACGGCTAATGATAAT
00443_1003_0754_D2	107502	R	AAAACCATGCAGATGCTAACCAAAGCTAACGCATTACCGAAACT
00454_1257_3047	59038	R	TGTTGCTGCATCATAATTAAATACATCATTCATTAAATCTTGG
00454_1257_3047_D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAATGCCCTAAACACAAAAGAT

Figure 15

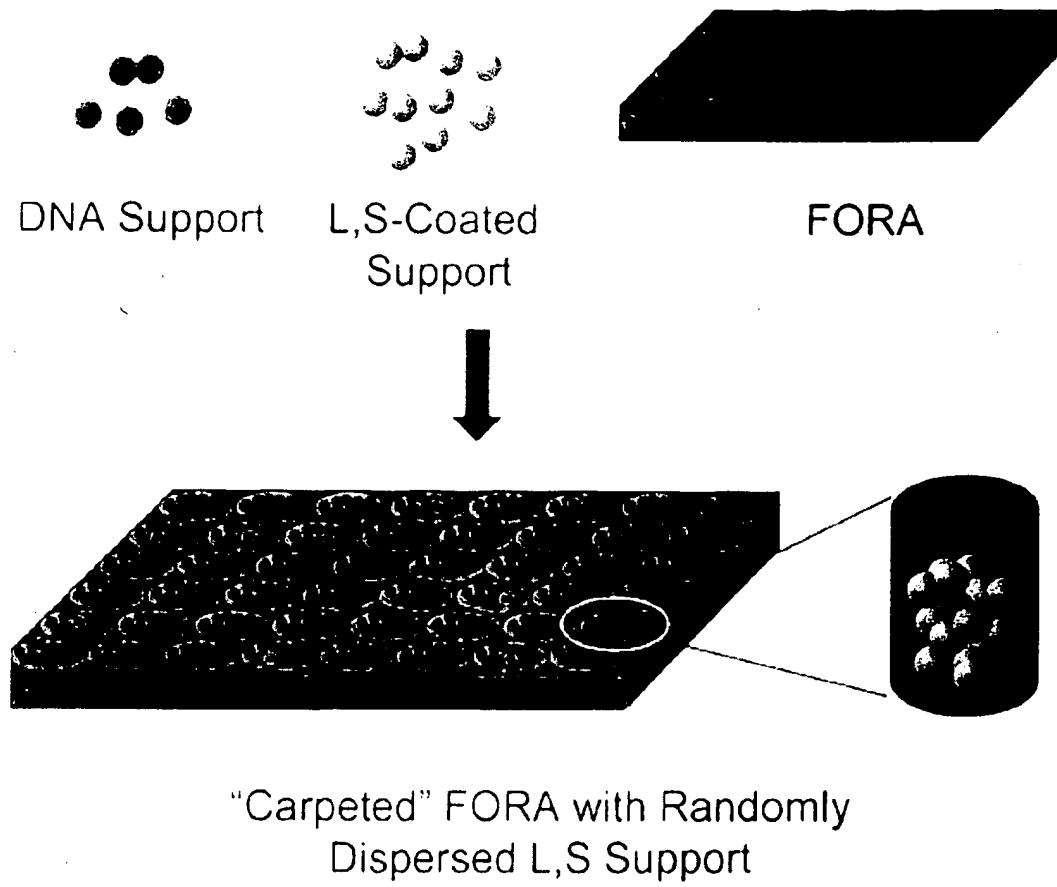


Figure 14

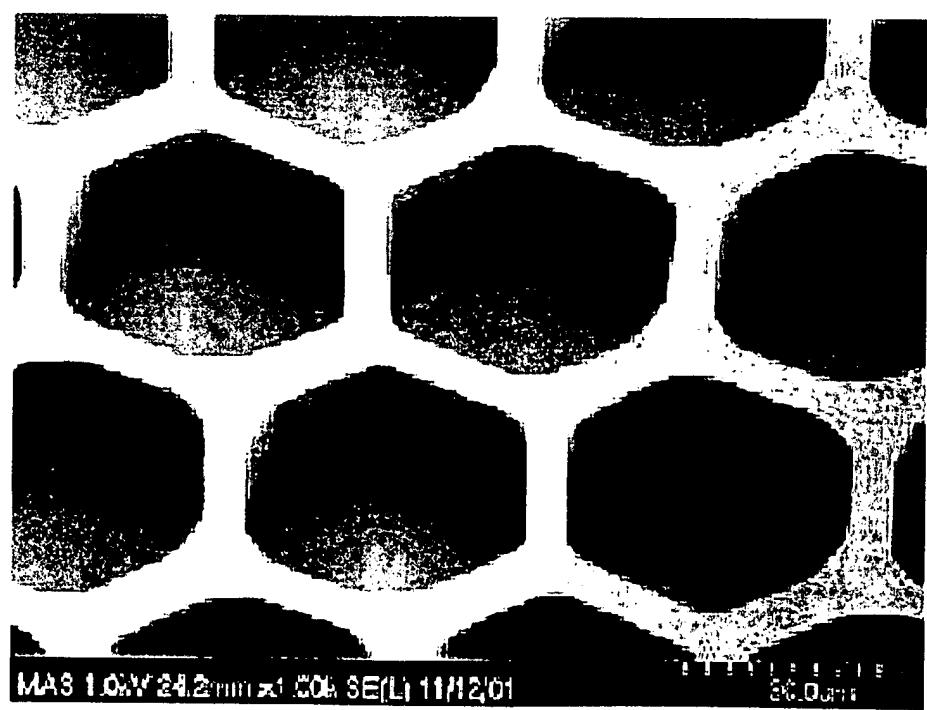
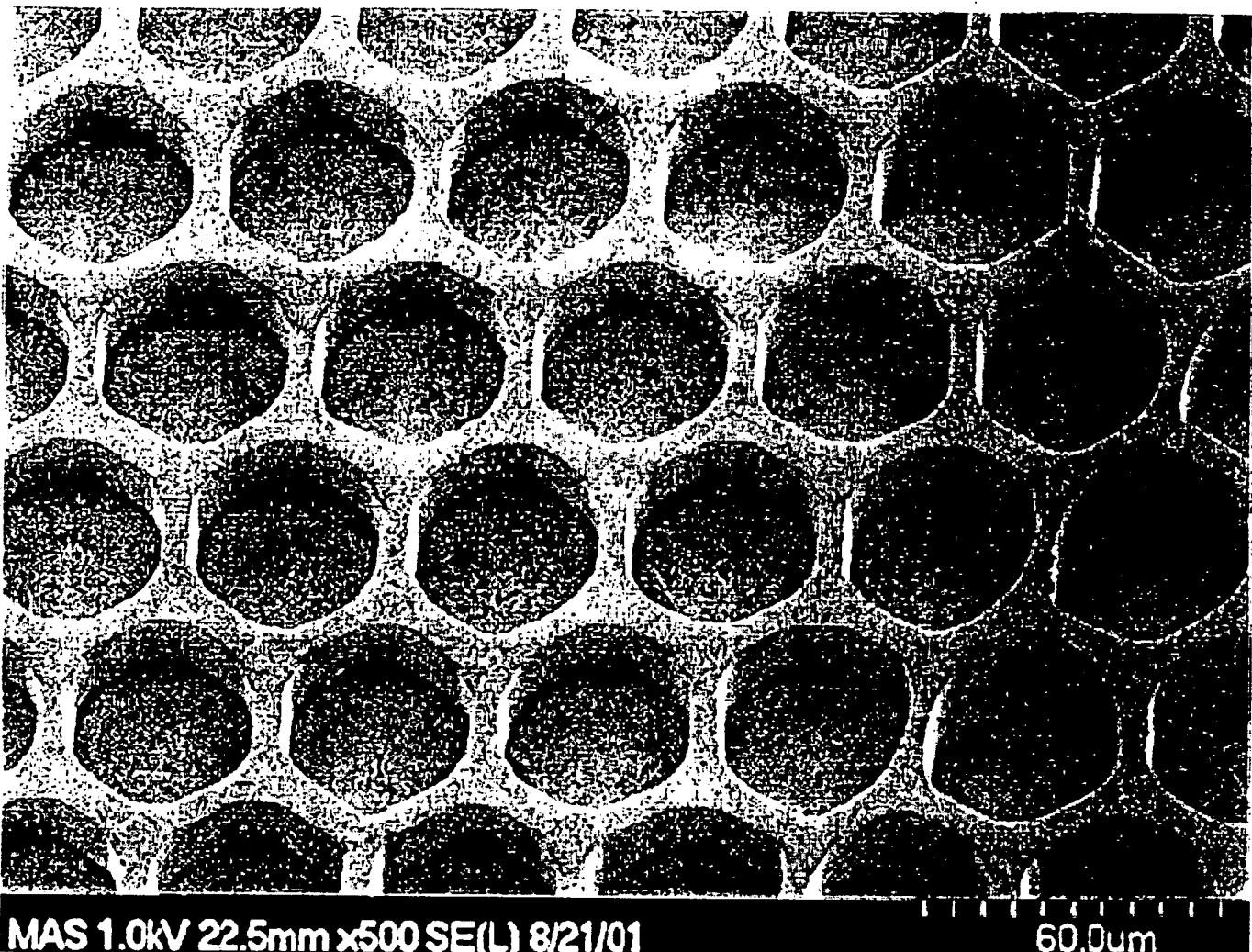


Figure 13

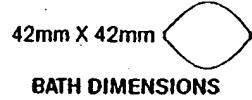
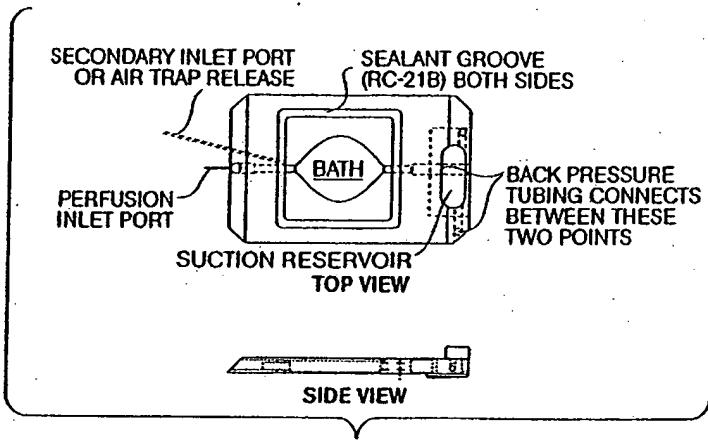
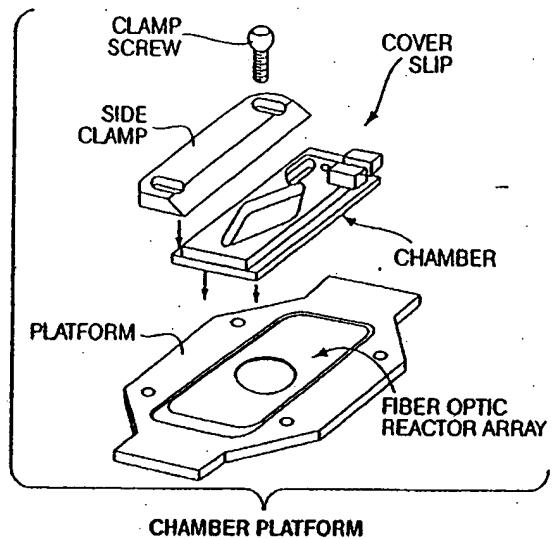


Fig. 3

Figure 12

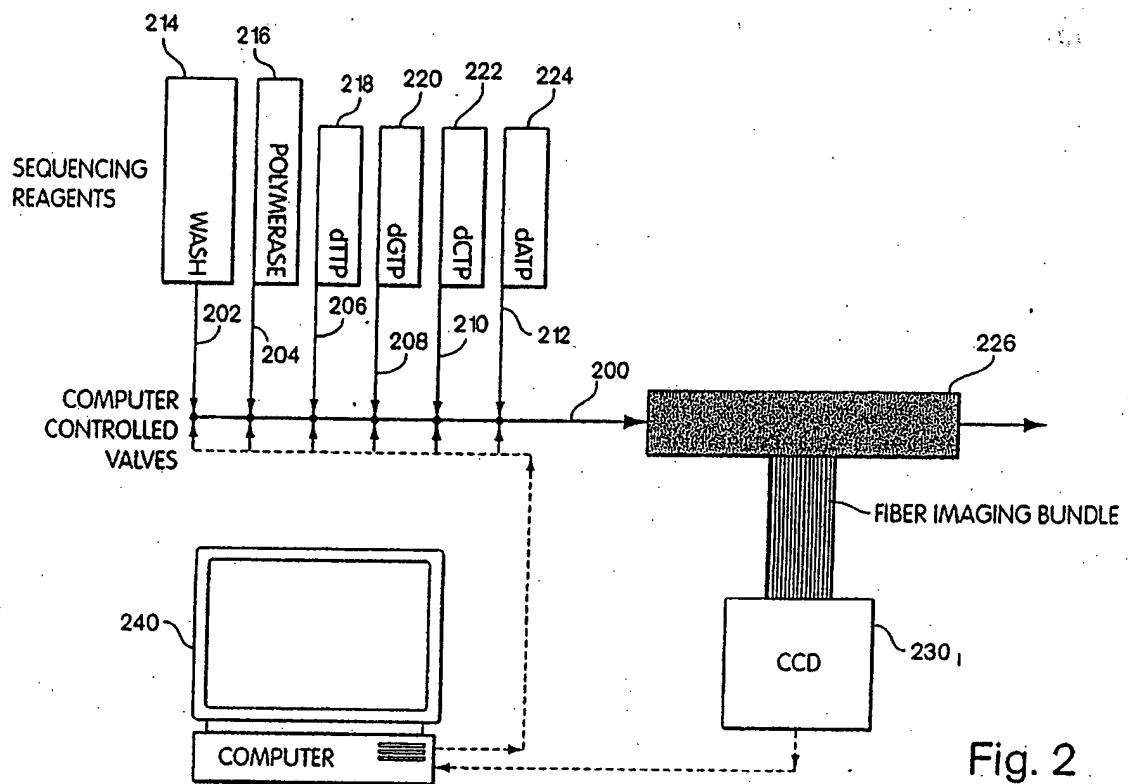


Fig. 2

Figure 11A

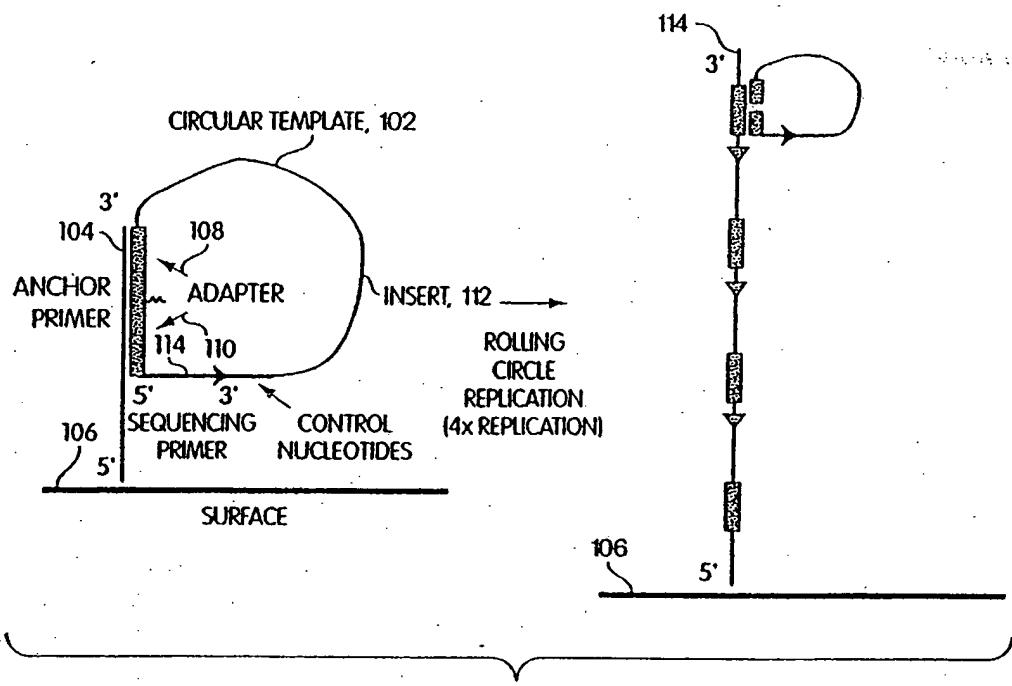


Figure 11B

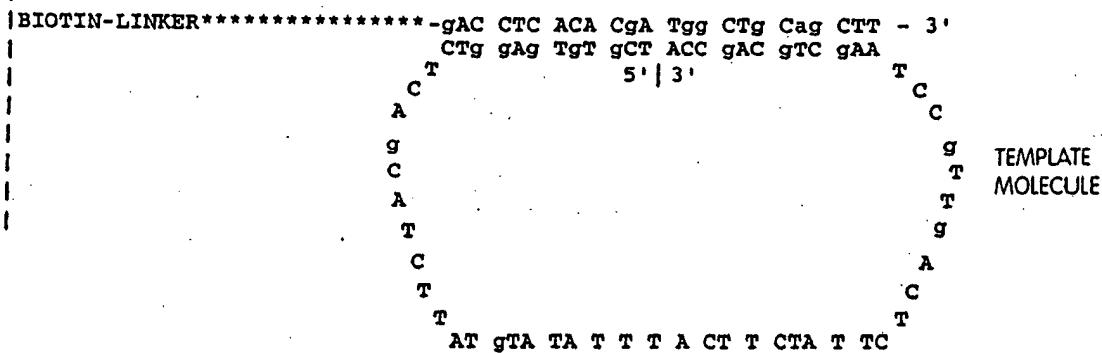
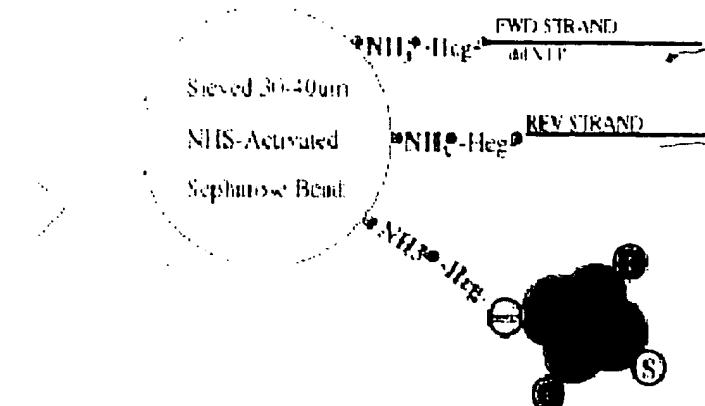
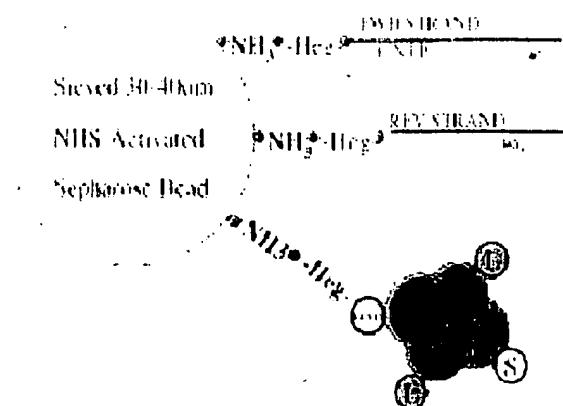
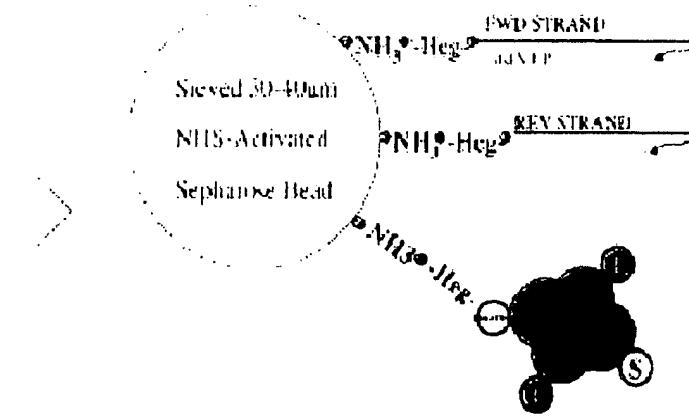
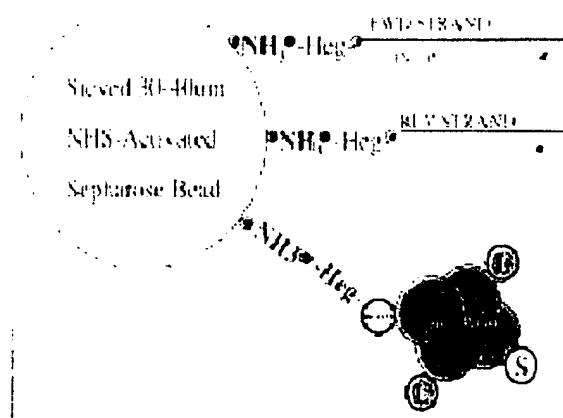


Fig. 1B

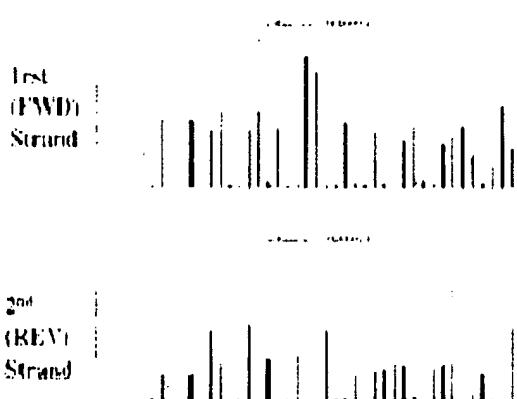
D.)



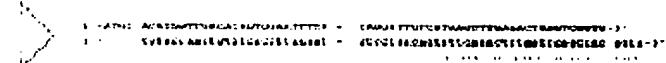
E.)



F.)



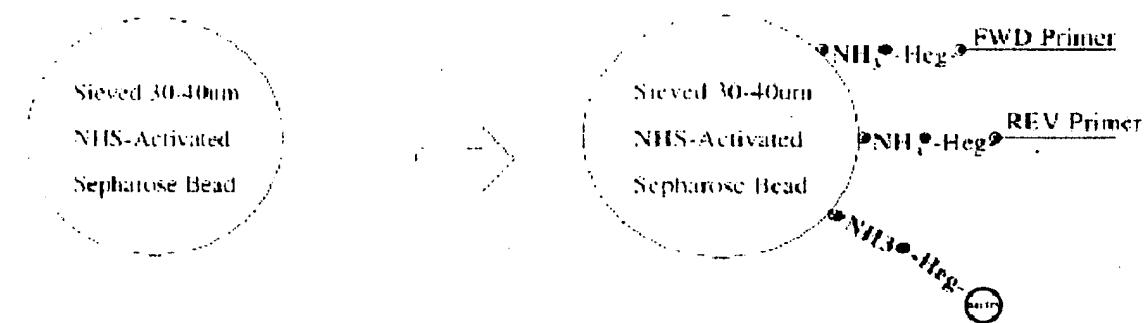
Sample	Initial Length	Stress	Percent Stretch Length
PE-14-1	0.03333333333333333	1.0	1.0
PE-14-2	0.03333333333333333	1.0	1.0



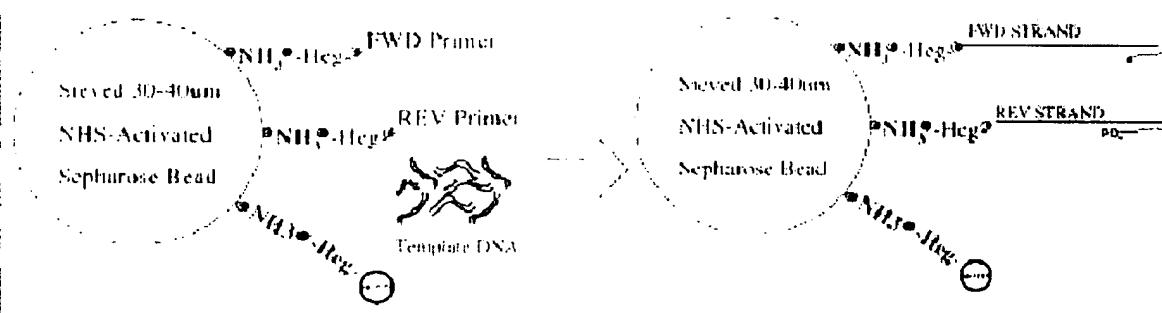
Part No	Weld Location	Suspension	Parted Match Length
TC-14-1	Welded	Welded	100mm

FIGURE 10

A.)



B.)



C.)

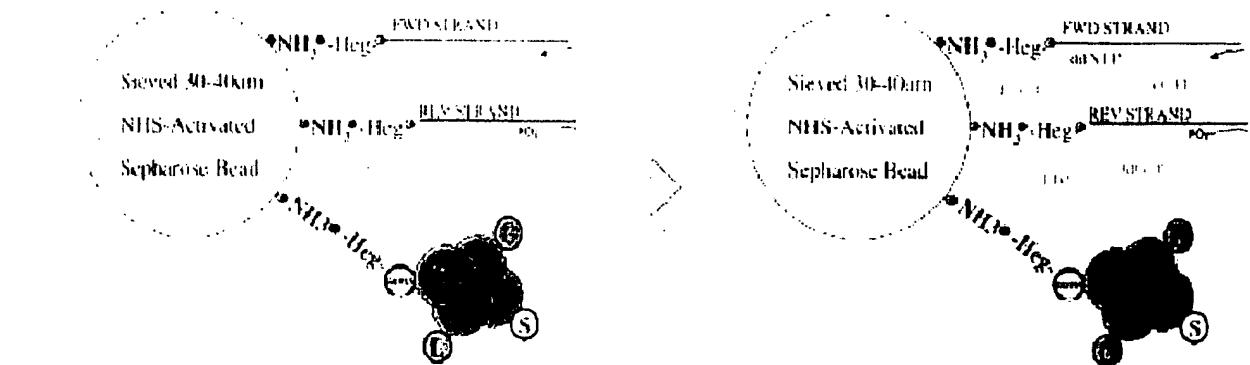
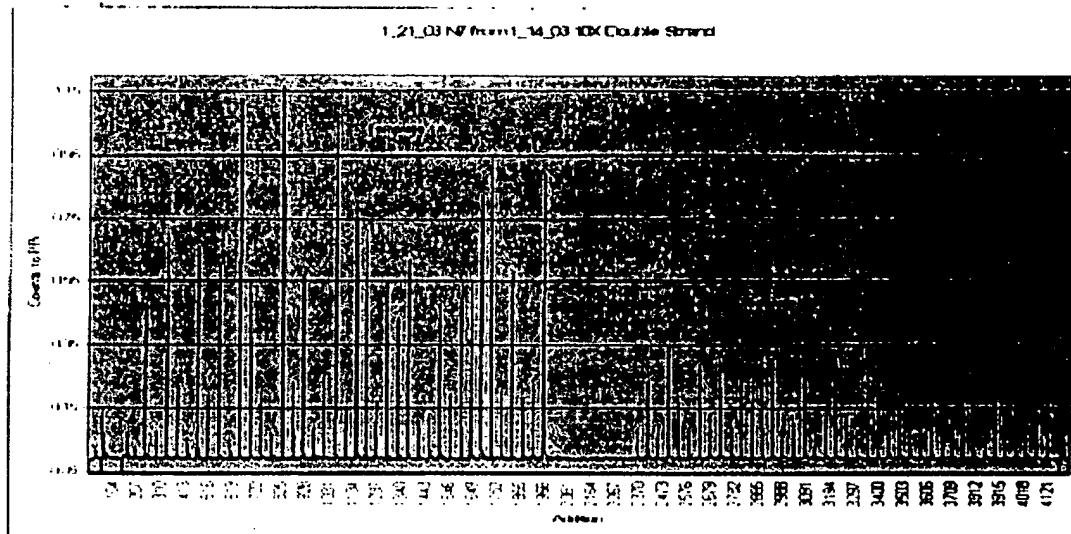


FIGURE 9



NYC 261535v2

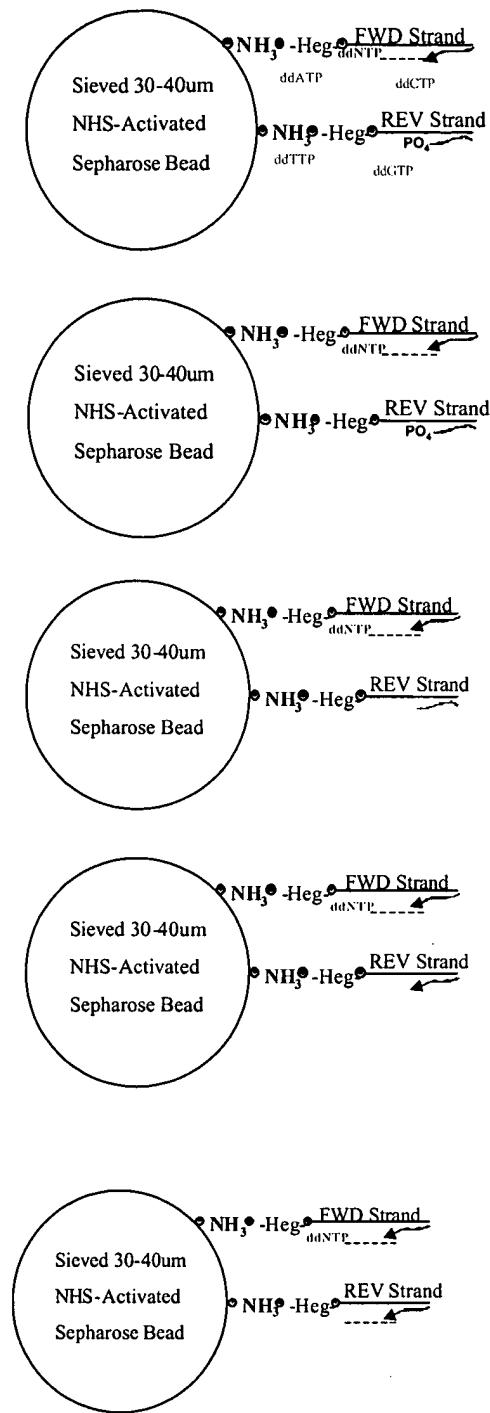


FIGURE 8

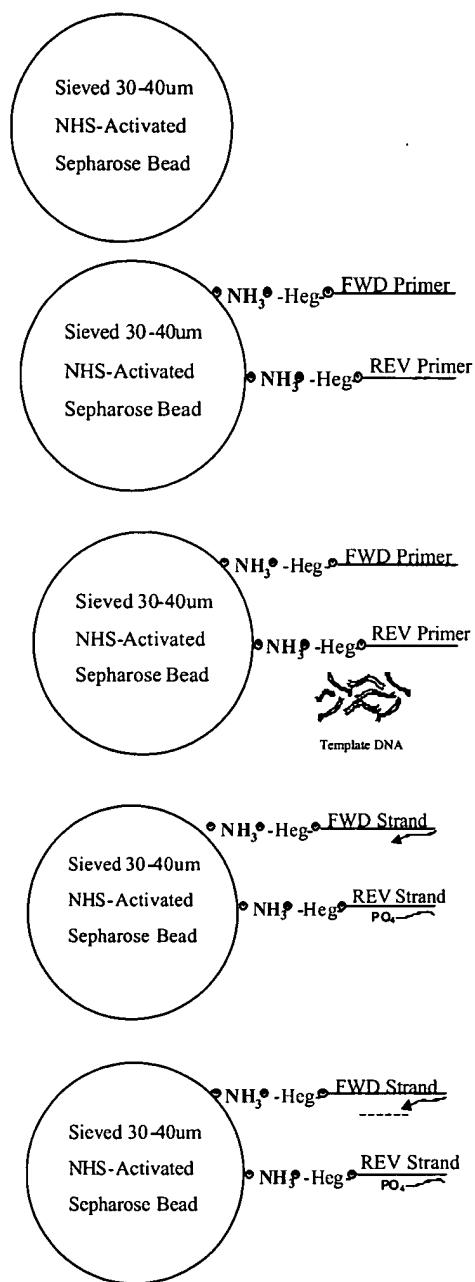


FIGURE 7

## Schematic Process Flow for Bead Separation

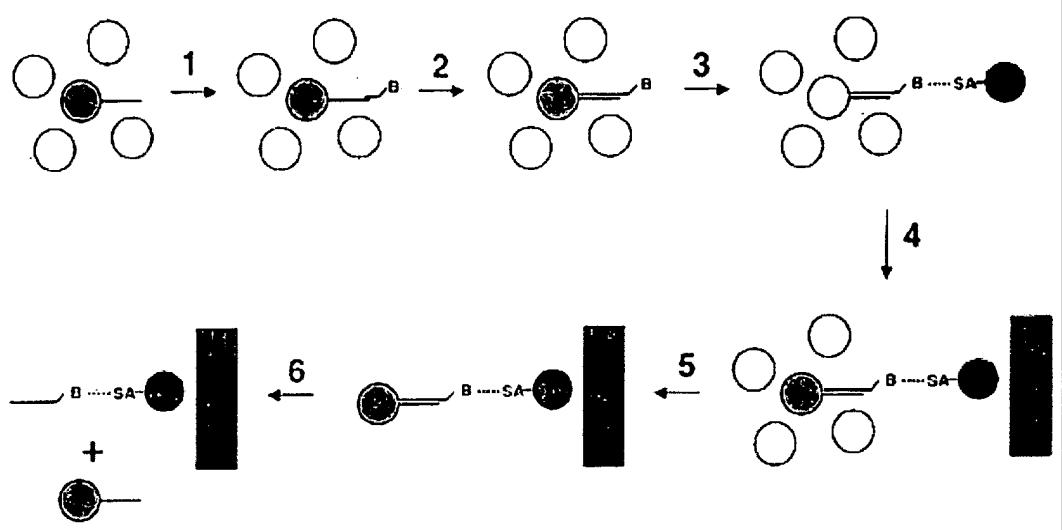


FIGURE 6B

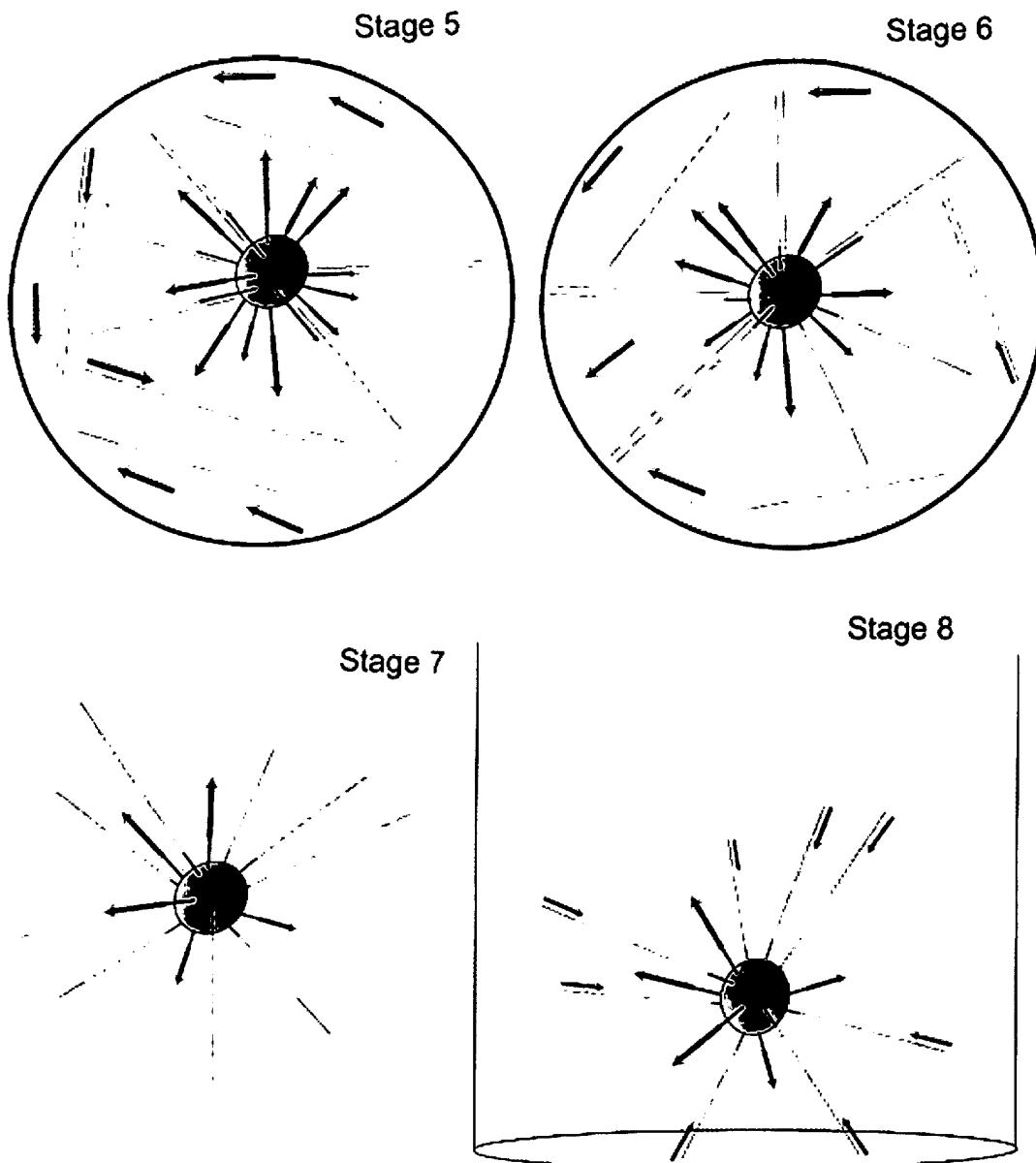


FIGURE 6A

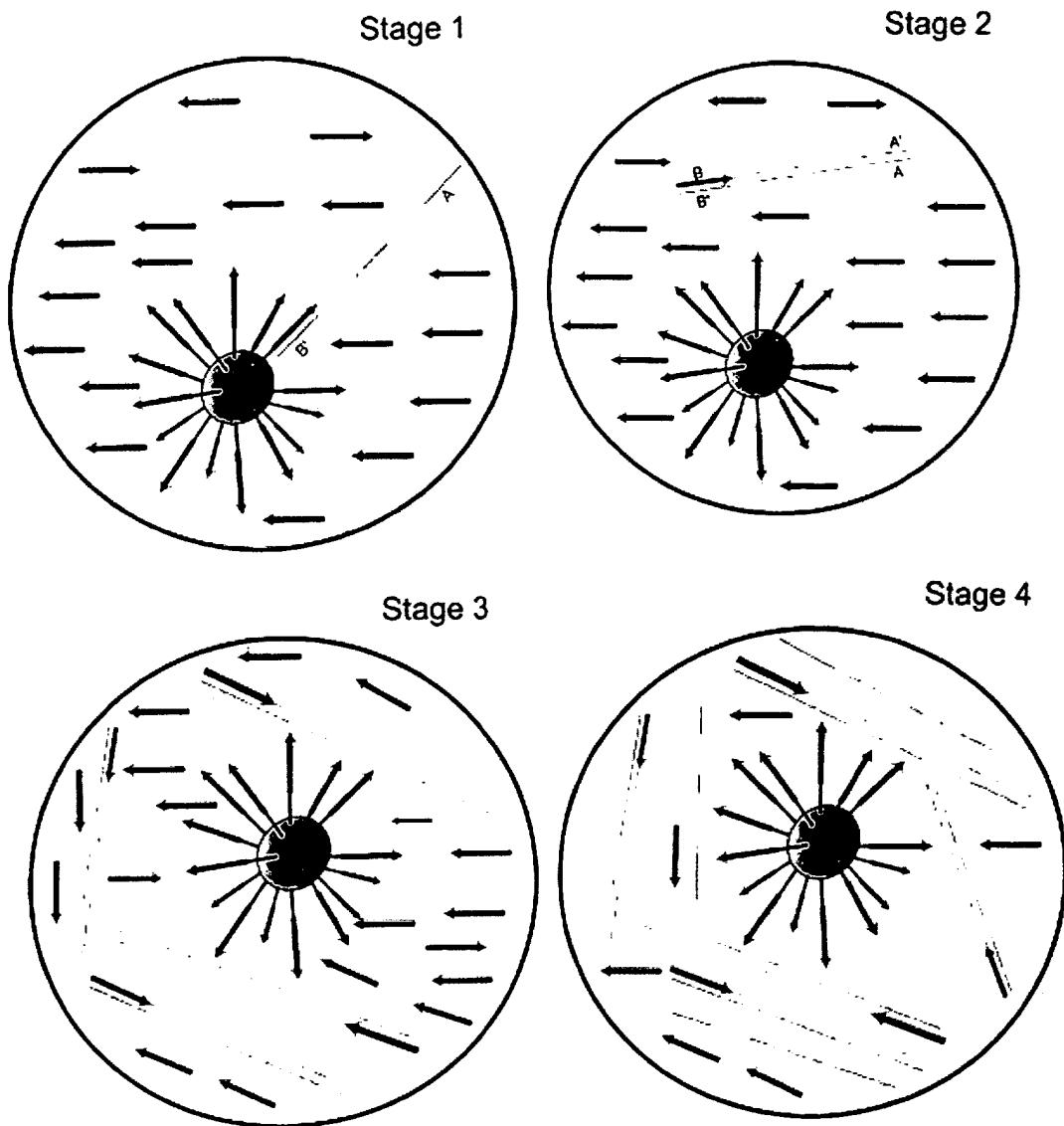


Figure 5

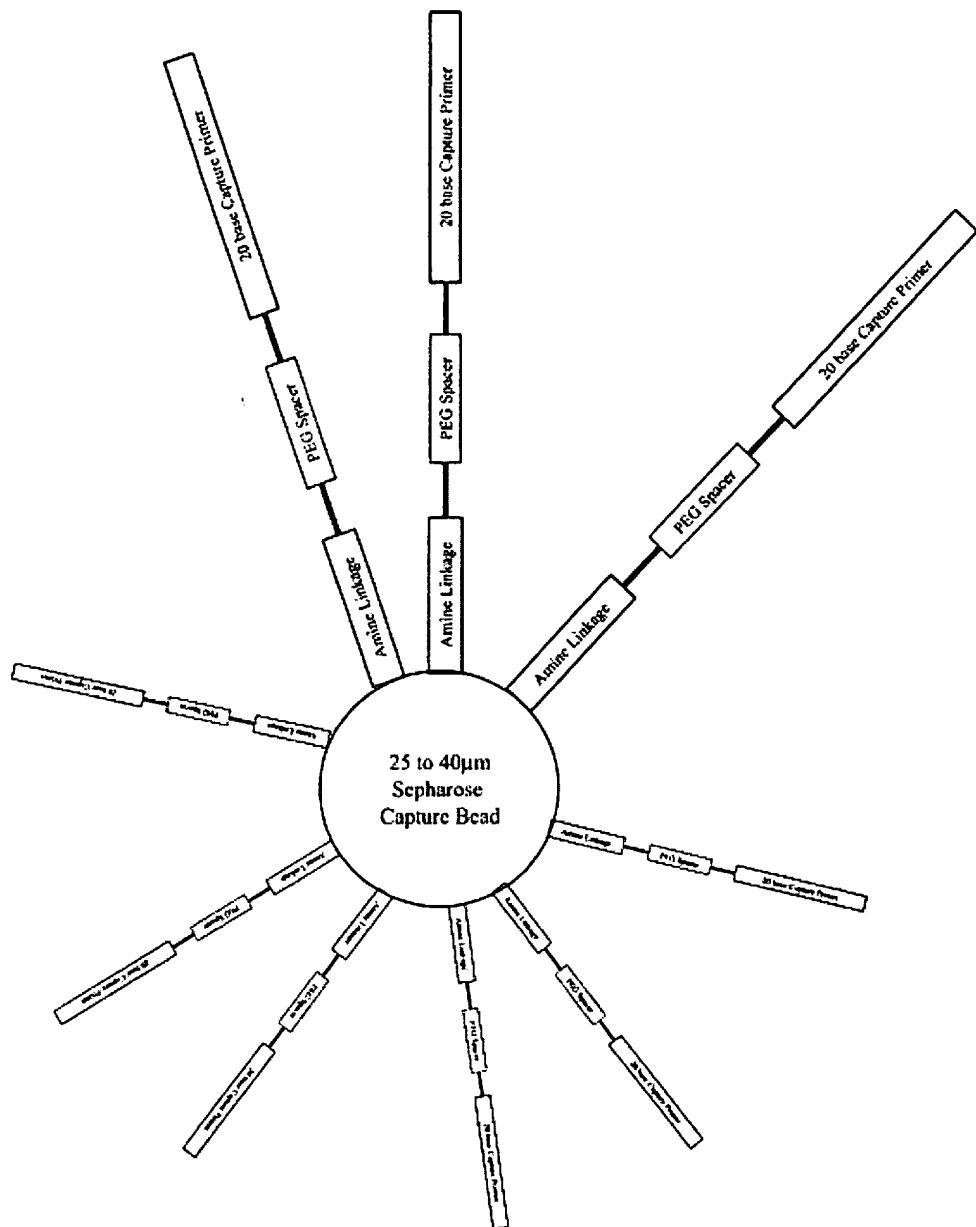
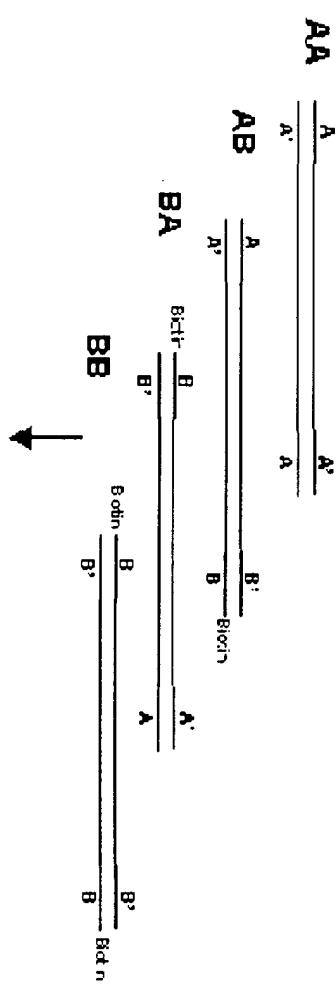


Figure 4

### Possible double-stranded Genomic DNA Library Species:



**AB, BA: Single end bound**  
ssDNA strand are released  
in the presence of a wash set  
net solution

**AA:** Unbound  
washed away

**BB: Both ends bound**  
remain on bead

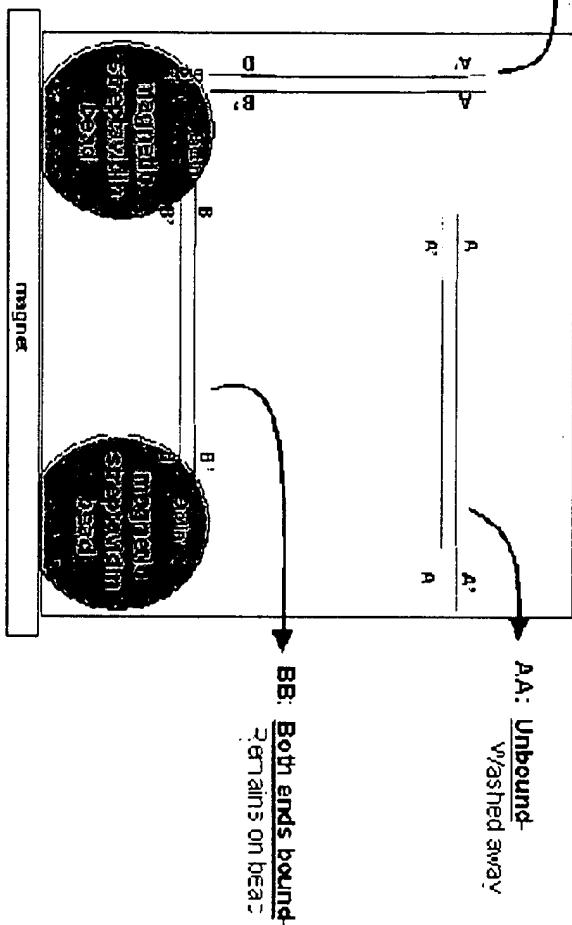


Figure 3

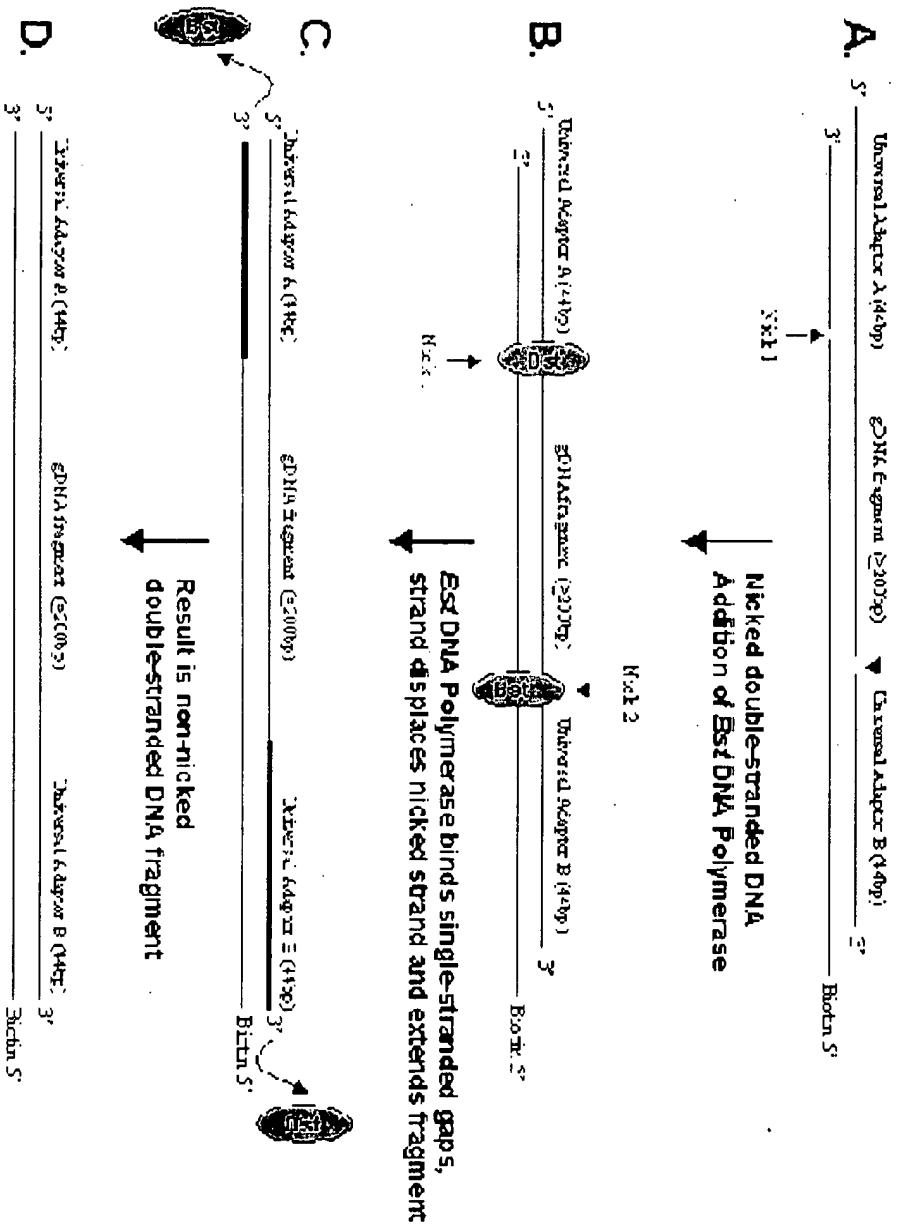


Figure 2A

### Universal Adaptor A

### Universal Adaptor B

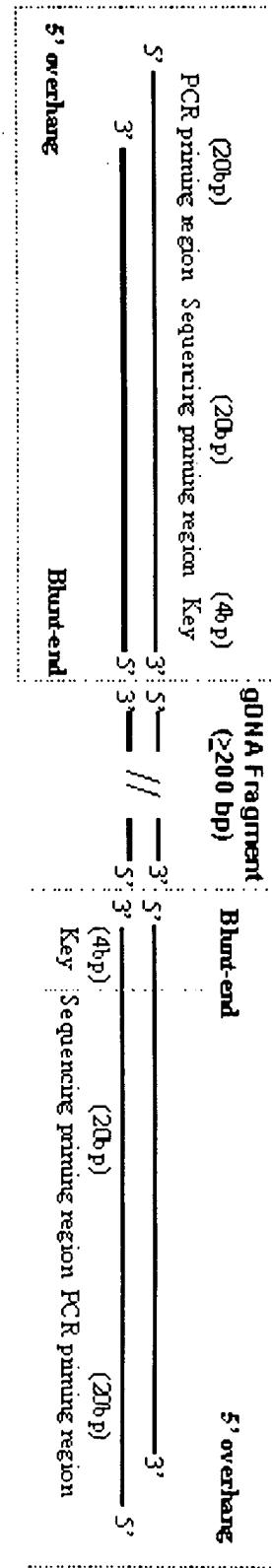


Figure 2B

### Adaptor A

MMP1A	MMP7A	Key	DNA fragment
5' cgtttccctgtgccttg -ccatctgttccctccctgtc-atgc -	3' --- 5'	-gcat -gacacgcacaggatagg -gacacgcacgcaacag	3'
3' agggacacacgaaac -ggtagacaaggagggacag -tacg -	5' --- 3'	-cgta -ctgtgcgttgtccctatcc -ctgtgcgtgcgtgtctacc -Biotin	
	Key	MMP2B	MMP1B

### Adaptor B

Figure 2C

(4 base 5' overhang) Adaptor A                          DNA fragment                          Adaptor B (4 base 5' overhang)

**Sense Strand** 5' [PCR primer (20 bp)-Seq Primer (20 bp)- Key (4 bp)] DNA Fragment [key (4 bp)-Seq Primer (20 bp)-PCR primer (20 bp)] 3'  
**Anti Strand** 3' [PCR primer (20 bp)- Seq Primer (20 bp)- Key (4 bp)] DNA Fragment [key (4 bp)-Seq Primer (20 bp)-PCR primer (20 bp)] 5' (**BEAD**)

454

## The 454 Sequencing system

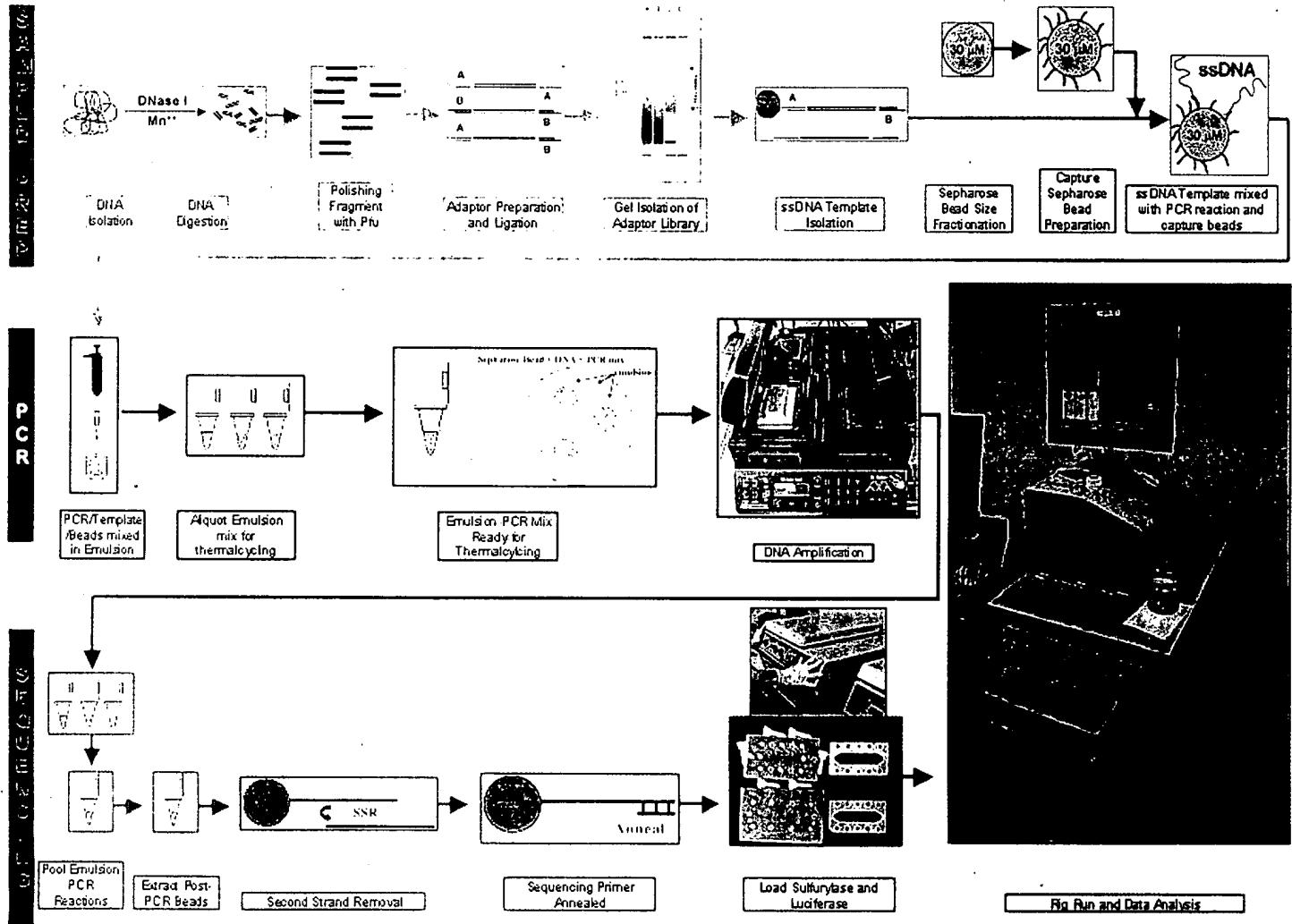


Figure 1F

A B C D E

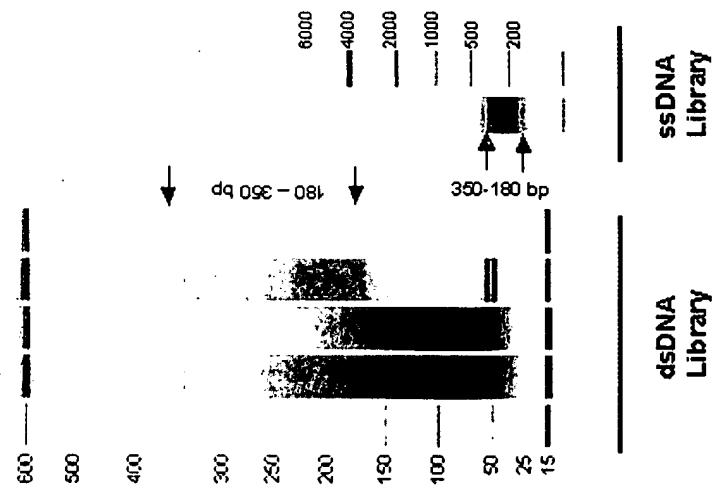


Figure 1A.

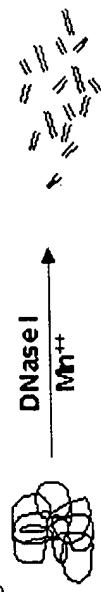


Figure 1B.

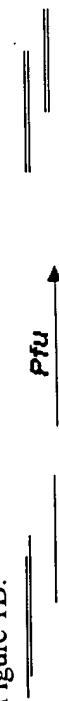


Figure 1C.



Figure 1D.

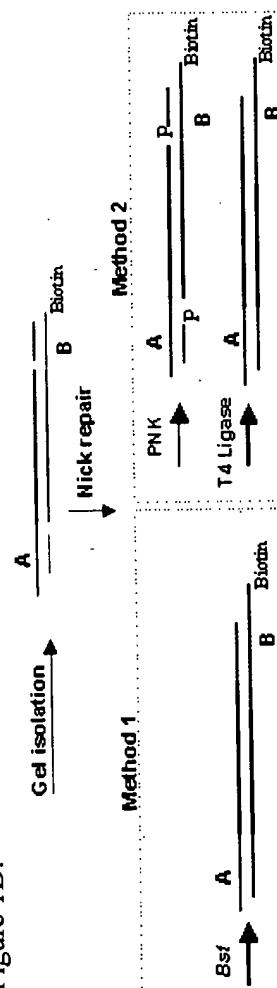
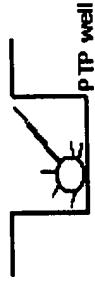


Figure 1E

**B**ind non-nicked dsDNA to streptavidin-coated beads and single strand elution

Bind to Sepharose DNA Capture Bead (1 ssDNA A per bead)

**D**eposition of a single DNA Capture Bead per well



Amplification  
Sequence